

PCT

WORLD INTELLECTUAL PROPERTY ORGANIZATION
International Bureau

INTERNATIONAL APPLICATION PUBLISHED UNDER THE PATENT COOPERATION TREATY (PCT)

(51) International Patent Classification 6 : G01N 33/574, 33/577, C07K 16/30, A61K 39/395, 47/48, C12Q 1/68, G01N 33/543		A2	(11) International Publication Number: WO 98/37418
			(43) International Publication Date: 27 August 1998 (27.08.98)
(21) International Application Number: PCT/US98/03690		(81) Designated States: AL, AM, AT, AU, BA, BB, BG, BR, BY, CA, CH, CN, CU, CZ, DE, DK, EE, ES, FI, GB, GE, GH, GM, GW, HU, ID, IL, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, UA, UG, UZ, VN, YU, ZW, ARIPO patent (GH, GM, KE, LS, MW, SD, SZ, UG, ZW), Eurasian patent (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European patent (AT, BE, CH, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE), OAPI patent (BF, BJ, CF, CG, CI, CM, GA, GN, ML, MR, NE, SN, TD, TG).	
(22) International Filing Date: 25 February 1998 (25.02.98)		Published <i>Without international search report and to be republished upon receipt of that report.</i>	
(30) Priority Data: 08/806,596 25 February 1997 (25.02.97) US 08/904,809 1 August 1997 (01.08.97) US Not furnished 9 February 1998 (09.02.98) US			
(71) Applicant: CORIXA CORPORATION [US/US]; Suite 200, 1124 Columbia Street, Seattle, WA 98104 (US).			
(72) Inventors: XU, Jiangchun; 15805 Southeast 43rd Place, Bellevue, WA 98006 (US). DILLON, Davin, C.; 21607 N.E. 24th Street, Redmond, WA 98053 (US).			
(74) Agents: MAKI, David, J. et al.; Seed and Berry LLP, 6300 Columbia Center, 701 Fifth Avenue, Seattle, WA 98104-7092 (US).			

(54) Title: COMPOUNDS FOR IMMUNODIAGNOSIS OF PROSTATE CANCER AND METHODS FOR THEIR USE

(57) Abstract

Compounds and methods for diagnosing prostate cancer are provided. The inventive compounds include polypeptides containing at least a portion of a prostate tumor protein. The inventive polypeptides may be used to generate antibodies useful for the diagnosis and monitoring of prostate cancer. Nucleic acid sequences for preparing probes, primers, and polypeptides are also provided.

09/825, 294 #5

FOR THE PURPOSES OF INFORMATION ONLY

Codes used to identify States party to the PCT on the front pages of pamphlets publishing international applications under the PCT.

AL	Albania	ES	Spain	LS	Lesotho	SI	Slovenia
AM	Armenia	FI	Finland	LT	Lithuania	SK	Slovakia
AT	Austria	FR	France	LU	Luxembourg	SN	Senegal
AU	Australia	GA	Gabon	LV	Latvia	SZ	Swaziland
AZ	Azerbaijan	GB	United Kingdom	MC	Moscow	TD	Chad
BA	Bosnia and Herzegovina	GE	Georgia	MD	Republic of Moldova	TG	Togo
BB	Barbados	GH	Ghana	MG	Madagascar	TJ	Tajikistan
BE	Belgium	GN	Guinea	MK	The former Yugoslav	TM	Turkmenistan
BF	Burkina Faso	GR	Greece	ML	Republic of Macedonia	TR	Turkey
BG	Bulgaria	HU	Hungary	MN	Mali	TT	Trinidad and Tobago
BJ	Benin	IE	Ireland	MR	Mauritania	UA	Ukraine
BR	Brazil	IL	Israel	MW	Malawi	UG	Uganda
BV	Belarus	IS	Iceland	MX	Mexico	US	United States of America
CA	Canada	IT	Italy	NK	Niger	UZ	Uzbekistan
CF	Central African Republic	JP	Japan	NL	Netherlands	VN	Viet Nam
CG	Congo	KE	Kenya	NO	Norway	YU	Yugoslavia
CH	Switzerland	KG	Kyrgyzstan	NZ	New Zealand	ZW	Zimbabwe
CI	Côte d'Ivoire	KP	Democratic People's Republic of Korea	PL	Poland		
CM	Cameroon	KR	Republic of Korea	PT	Portugal		
CN	China	KZ	Republic of Korea	RO	Romania		
CU	Cuba	LC	Kazakhstan	RU	Russian Federation		
CZ	Czech Republic	LI	Saint Lucia	SD	Sudan		
DE	Germany	LK	Liechtenstein	SE	Sweden		
DK	Denmark	LR	Sri Lanka	SG	Singapore		
EE	Estonia		Liberia				

238 P3

COMPOUNDS FOR IMMUNODIAGNOSIS OF PROSTATE CANCER AND METHODS FOR THEIR USE

TECHNICAL FIELD

The present invention relates generally to the treatment and monitoring of prostate cancer. The invention is more particularly related to polypeptides comprising at least a portion of a prostate protein. Such polypeptides may be used for the production of compounds, such as antibodies, useful for diagnosing and monitoring the progression of prostate cancer, and possibly other tumor types, in a patient.

BACKGROUND OF THE INVENTION

Prostate cancer is the most common form of cancer among males, with an estimated incidence of 30% in men over the age of 50. Overwhelming clinical evidence shows that human prostate cancer has the propensity to metastasize to bone, and the disease appears to progress inevitably from androgen dependent to androgen refractory status, leading to increased patient mortality. This prevalent disease is currently the second leading cause of cancer death among men in the U.S.

In spite of considerable research into diagnosis and therapy of the disease, prostate cancer remains difficult to detect and to treat. Commonly, treatment is based on surgery and/or radiation therapy, but these methods are ineffective in a significant percentage of cases. Two previously identified prostate specific proteins - prostate specific antigen (PSA) and prostatic acid phosphatase (PAP) - have limited diagnostic and therapeutic potential. For example, PSA levels do not always correlate well with the presence of prostate cancer, being positive in a percentage of non-prostate cancer cases, including benign prostatic hyperplasia (BPH). Furthermore, PSA measurements correlate with prostate volume, and do not indicate the level of metastasis.

Accordingly, there remains a need in the art for improved and diagnostic methods for prostate cancer.

SUMMARY OF THE INVENTION

The present invention provides methods for immunodiagnosis of prostate cancer, together with kits for use in such methods. Polypeptides are disclosed which comprise at least an immunogenic portion of a prostate tumor protein or a variant of said protein that differs only in conservative substitutions and/or modifications, wherein the prostate tumor protein comprises an amino acid sequence encoded by a DNA molecule having a sequence selected from the group consisting of nucleotide sequences recited in SEQ ID Nos: 2-3, 5-107, 109-11, 115-171, 173-175, 177, 179-224 and variants thereof. Such polypeptides may be usefully employed in the diagnosis and monitoring of prostate cancer.

In one specific aspect of the present invention, methods are provided for detecting prostate cancer in a patient, comprising: (a) contacting a biological sample obtained from a patient with a binding agent that is capable of binding to one of the above polypeptides; and (b) detecting in the sample a protein or polypeptide that binds to the binding agent. In preferred embodiments, the binding agent is an antibody, most preferably a monoclonal antibody.

In related aspects, methods are provided for monitoring the progression of prostate cancer in a patient, comprising: (a) contacting a biological sample obtained from a patient with a binding agent that is capable of binding to one of the above polypeptides; (b) determining in the sample an amount of a protein or polypeptide that binds to the binding agent; (c) repeating steps (a) and (b); and comparing the amounts of polypeptide detected in steps (b) and (c).

Within related aspects, the present invention provides antibodies, preferably monoclonal antibodies, that bind to the inventive polypeptides, as well as diagnostic kits comprising such antibodies, and methods of using such antibodies to inhibit the development of prostate cancer.

The present invention further provides methods for detecting prostate cancer comprising: (a) obtaining a biological sample from a patient; (b) contacting the sample with a first and a second oligonucleotide primer in a polymerase chain reaction, at least one of the oligonucleotide primers being specific for a DNA molecule that encodes one of the above polypeptides; and (c) detecting in the sample a DNA sequence that amplifies in the presence of the first and second oligonucleotide primers. In a preferred embodiment, at least one of the

oligonucleotide primers comprises at least about 10 contiguous nucleotides of a DNA molecule having a partial sequence selected from the group consisting of SEQ ID Nos: 2-3, 5-107, 109-11, 115-171, 173-175, 177 and 179-224.

In a further aspect, the present invention provides a method for detecting prostate cancer in a patient comprising: (a) obtaining a biological sample from the patient; (b) contacting the sample with an oligonucleotide probe specific for a DNA molecule that encodes one of the above polypeptides; and (c) detecting in the sample a DNA sequence that hybridizes to the oligonucleotide probe. Preferably, the oligonucleotide probe comprises at least about 15 contiguous nucleotides of a DNA molecule having a partial sequence selected from the group consisting of SEQ ID Nos: 2-3, 5-107, 109-11, 115-171, 173-175, 177 and 179-224.

In related aspects, diagnostic kits comprising the above oligonucleotide probes or primers are provided.

These and other aspects of the present invention will become apparent upon reference to the following detailed description and attached drawings. All references disclosed herein are hereby incorporated by reference in their entirety as if each was incorporated individually.

DETAILED DESCRIPTION OF THE INVENTION

As noted above, the present invention is generally directed to compositions and methods for the immunodiagnosis and monitoring of prostate cancer. The inventive compositions are generally polypeptides that comprise at least a portion of a prostate tumor protein. Also included within the present invention are molecules (such as an antibody or fragment thereof) that bind to the inventive polypeptides. Such molecules are referred to herein as "binding agents."

In particular, the subject invention discloses polypeptides comprising at least a portion of a human prostate tumor protein, or a variant thereof such a protein, wherein the prostate tumor protein includes an amino acid sequence encoded by a DNA molecule having a sequence selected from the group consisting of nucleotide sequences recited in SEQ ID Nos: 2-3, 5-107, 109-11, 115-171, 173-175, 177, 179-224, the complements of said nucleotide sequences and variants thereof. As used herein, the term "polypeptide"

encompasses amino acid chains of any length, including full length proteins, wherein the amino acid residues are linked by covalent peptide bonds. Thus, a polypeptide comprising a portion of one of the above prostate proteins may consist entirely of the portion, or the portion may be present within a larger polypeptide that contains additional sequences. The additional sequences may be derived from the native protein or may be heterologous, and such sequences may be immunoreactive and/or antigenic.

As used herein, an "immunogenic portion" of a human prostate tumor protein is a portion that is capable of eliciting an immune response in a patient inflicted with prostate cancer and as such binds to antibodies present within sera from a prostate cancer patient. Immunogenic portions of the proteins described herein may thus be identified in antibody binding assays. Such assays may generally be performed using any of a variety of means known to those of ordinary skill in the art, as described, for example, in Harlow and Lane, *Antibodies: A Laboratory Manual*, Cold Spring Harbor Laboratory, Cold Spring Harbor, NY, 1988. For example, a polypeptide may be immobilized on a solid support (as described below) and contacted with patient sera to allow binding of antibodies within the sera to the immobilized polypeptide. Unbound sera may then be removed and bound antibodies detected using, for example, ¹²⁵I-labeled Protein A. Alternatively, a polypeptide may be used to generate monoclonal and polyclonal antibodies for use in detection of the polypeptide in blood or other fluids of prostate cancer patients.

The compositions and methods of the present invention also encompass variants of the above polypeptides and DNA molecules. A polypeptide "variant," as used herein, is a polypeptide that differs from the recited polypeptide only in conservative substitutions and/or modifications, such that the therapeutic, antigenic and/or immunogenic properties of the polypeptide are retained. Polypeptide variants preferably exhibit at least about 70%, more preferably at least about 90% and most preferably at least about 95% identity to the identified polypeptides. For prostate tumor polypeptides with immunoreactive properties, variants may, alternatively, be identified by modifying the amino acid sequence of one of the above polypeptides, and evaluating the immunoreactivity of the modified polypeptide. For prostate tumor polypeptides useful for the generation of diagnostic binding agents, a variant may be identified by evaluating a modified polypeptide for the ability to

generate antibodies that detect the presence or absence of prostate cancer. Such modified sequences may be prepared and tested using, for example, the representative procedures described herein.

As used herein, a "conservative substitution" is one in which an amino acid is substituted for another amino acid that has similar properties, such that one skilled in the art of peptide chemistry would expect the secondary structure and hydrophobic nature of the polypeptide to be substantially unchanged. In general, the following groups of amino acids represent conservative changes: (1) ala, pro, gly, glu, asp, gln, asn; ser, thr; (2) cys, ser, tyr, thr; (3) val, ile, leu, met, ala, phe; (4) lys, arg, his; and (5) phe, tyr, trp, his.

Variants may also, or alternatively, contain other modifications, including the deletion or addition of amino acids that have minimal influence on the antigenic properties, secondary structure and hydrophobic nature of the polypeptide. For example, a polypeptide may be conjugated to a signal (or leader) sequence at the N-terminal end of the protein which co-translationally or post-translationally directs transfer of the protein. The polypeptide may also be conjugated to a linker or other sequence for ease of synthesis, purification or identification of the polypeptide (e.g., poly-His), or to enhance binding of the polypeptide to a solid support. For example, a polypeptide may be conjugated to an immunoglobulin Fc region.

A nucleotide "variant" is a sequence that differs from the recited nucleotide sequence in having one or more nucleotide deletions, substitutions or additions. Such modifications may be readily introduced using standard mutagenesis techniques, such as oligonucleotide-directed site-specific mutagenesis as taught, for example, by Adelman et al. (DNA, 2:183, 1983). Nucleotide variants may be naturally occurring allelic variants, or non-naturally occurring variants. Variant nucleotide sequences preferably exhibit at least about 70%, more preferably at least about 80% and most preferably at least about 90% identity to the recited sequence. Such variant nucleotide sequences will generally hybridize to the recited nucleotide sequence under stringent conditions. As used herein, "stringent conditions" refers to prewashing in a solution of 6X SSC, 0.2% SDS; hybridizing at 65 °C, 6X SSC, 0.2% SDS overnight; followed by two washes of 30 minutes each in 1X SSC, 0.1% SDS at 65 °C and two washes of 30 minutes each in 0.2X SSC, 0.1% SDS at 65 °C.

"Polypeptides" as used herein also include combination, or fusion, polypeptides. A "combination polypeptide" is a polypeptide comprising at least one of the above immunogenic portions and one or more additional immunogenic prostate tumor-specific sequences, which are joined via a peptide linkage into a single amino acid chain. The sequences may be joined directly (*i.e.*, with no intervening amino acids) or may be joined by way of a linked sequence (*e.g.*, Gly-Cys-Gly) that does not significantly diminish the immunogenic properties of the component polypeptides.

The prostate tumor proteins of the present invention, and DNA molecules encoding such proteins, may be isolated from prostate tumor tissue using any of a variety of methods well known in the art. DNA sequences corresponding to a gene (or a portion thereof) encoding one of the inventive prostate tumor proteins may be isolated from a prostate tumor cDNA library using a subtraction technique as described in detail below. Examples of such DNA sequences are provided in SEQ ID Nos: 1-107, 109-111, 115-171, 173-175, 177 and 179-224. Partial DNA sequences thus obtained may be used to design oligonucleotide primers for the amplification of full-length DNA sequences in a polymerase chain reaction (PCR), using techniques well known in the art (see, for example, Mullis et al., *Cold Spring Harbor Symp. Quant. Biol.*, 51:263, 1987; Erlich ed., *PCR Technology*, Stockton Press, NY, 1989). Once a DNA sequence encoding a polypeptide is obtained, any of the above modifications may be readily introduced using standard mutagenesis techniques, such as oligonucleotide-directed site-specific mutagenesis as taught, for example, by Adelman et al. (*DNA*, 2:183, 1983).

The prostate tumor polypeptides disclosed herein may also be generated by synthetic or recombinant means. Synthetic polypeptides having fewer than about 100 amino acids, and generally fewer than about 50 amino acids, may be generated using techniques well known to those of ordinary skill in the art. For example, such polypeptides may be synthesized using any of the commercially available solid-phase techniques, such as the Merrifield solid-phase synthesis method, where amino acids are sequentially added to a growing amino acid chain (see, for example, Merrifield, *J. Am. Chem. Soc.* 85:2149-2146, 1963). Equipment for automated synthesis of polypeptides is commercially available from

suppliers such as Perkin Elmer/Applied BioSystems Division (Foster City, CA), and may be operated according to the manufacturer's instructions.

Alternatively, any of the above polypeptides may be produced recombinantly by inserting a DNA sequence that encodes the polypeptide into an expression vector and expressing the protein in an appropriate host. Any of a variety of expression vectors known to those of ordinary skill in the art may be employed to express recombinant polypeptides of this invention. Expression may be achieved in any appropriate host cell that has been transformed or transfected with an expression vector containing a DNA molecule that encodes a recombinant polypeptide. Suitable host cells include prokaryotes, yeast and higher eukaryotic cells. Preferably, the host cells employed are *E. coli*, yeast or a mammalian cell line, such as CHO cells. The DNA sequences expressed in this manner may encode naturally occurring polypeptides, portions of naturally occurring polypeptides, or other variants thereof.

In general, regardless of the method of preparation, the polypeptides disclosed herein are prepared in substantially pure form (*i.e.*, the polypeptides are homogenous as determined by amino acid composition and primary sequence analysis). Preferably, the polypeptides are at least about 90% pure, more preferably at least about 95% pure and most preferably at least about 99% pure. In certain embodiments, described in more detail below, the substantially pure polypeptides are incorporated into pharmaceutical compositions or vaccines for use in one or more of the methods disclosed herein.

In a related aspect, the present invention provides fusion proteins comprising a first and a second inventive polypeptide, or alternatively, a polypeptide of the present invention and a known prostate antigen, together with variants of such fusion proteins. The fusion proteins of the present invention may also include a linker peptide between the first and second polypeptides.

A DNA sequence encoding a fusion protein of the present invention is constructed using known recombinant DNA techniques to assemble separate DNA sequences encoding the first and second polypeptides into an appropriate expression vector. The 3' end of a DNA sequence encoding the first polypeptide is ligated, with or without a peptide linker, to the 5' end of a DNA sequence encoding the second polypeptide so that the reading frames

of the sequences are in phase to permit mRNA translation of the two DNA sequences into a single fusion protein that retains the biological activity of both the first and the second polypeptides.

A peptide linker sequence may be employed to separate the first and the second polypeptides by a distance sufficient to ensure that each polypeptide folds into its secondary and tertiary structures. Such a peptide linker sequence is incorporated into the fusion protein using standard techniques well known in the art. Suitable peptide linker sequences may be chosen based on the following factors: (1) their ability to adopt a flexible extended conformation; (2) their inability to adopt a secondary structure that could interact with functional epitopes on the first and second polypeptides; and (3) the lack of hydrophobic or charged residues that might react with the polypeptide functional epitopes. Preferred peptide linker sequences contain Gly, Asn and Ser residues. Other near neutral amino acids, such as Thr and Ala may also be used in the linker sequence. Amino acid sequences which may be usefully employed as linkers include those disclosed in Maratea et al., *Gene* 40:39-46, 1985; Murphy et al., *Proc. Natl. Acad. Sci., USA* 83:8258-8262, 1986; U.S. Patent No. 4,935,233 and U.S. Patent No. 4,751,180. The linker sequence may be from 1 to about 50 amino acids in length. Peptide sequences are not required when the first and second polypeptides have non-essential N-terminal amino acid regions that can be used to separate the functional domains and prevent steric interference.

The ligated DNA sequences are operably linked to suitable transcriptional or translational regulatory elements. The regulatory elements responsible for expression of DNA are located only 5' to the DNA sequence encoding the first polypeptides. Similarly, stop codons required to end translation and transcription termination signals are only present 3' to the DNA sequence encoding the second polypeptide.

Polypeptides and/or fusion proteins of the present invention may be used to generate binding agents, such as antibodies or fragments thereof, that are capable of detecting metastatic human prostate tumors. Binding agents of the present invention may generally be prepared using methods known to those of ordinary skill in the art, including the representative procedures described herein. Binding agents are capable of differentiating between patients with and without prostate cancer, using the representative assays described

herein. In other words, antibodies or other binding agents raised against a prostate tumor protein, or a suitable portion thereof, will generate a signal indicating the presence of primary or metastatic prostate cancer in at least about 20% of patients afflicted with the disease, and will generate a negative signal indicating the absence of the disease in at least about 90% of individuals without primary or metastatic prostate cancer. Suitable portions of such prostate tumor proteins are portions that are able to generate a binding agent that indicates the presence of primary or metastatic prostate cancer in substantially all (*i.e.*, at least about 80%, and preferably at least about 90%) of the patients for which prostate cancer would be indicated using the full length protein, and that indicate the absence of prostate cancer in substantially all of those samples that would be negative when tested with full length protein. The representative assays described below, such as the two antibody sandwich assay, may generally be employed for evaluating the ability of a binding agent to detect metastatic human prostate tumors.

The ability of a polypeptide and/or fusion protein prepared as described herein to generate antibodies capable of detecting primary or metastatic human prostate tumors may generally be evaluated by raising one or more antibodies against the polypeptide (using, for example, a representative method described herein) and determining the ability of such antibodies to detect such tumors in patients. This determination may be made by assaying biological samples from patients with and without primary or metastatic prostate cancer for the presence of a polypeptide that binds to the generated antibodies. Such test assays may be performed, for example, using a representative procedure described below. Polypeptides that generate antibodies capable of detecting at least 20% of primary or metastatic prostate tumors by such procedures are considered to be useful in assays for detecting primary or metastatic human prostate tumors. Polypeptide specific antibodies may be used alone or in combination to improve sensitivity.

Polypeptides and/or fusion proteins capable of detecting primary or metastatic human prostate tumors may be used as markers for diagnosing prostate cancer or for monitoring disease progression in patients. In one embodiment, prostate cancer in a patient may be diagnosed by evaluating a biological sample obtained from the patient for the level of

one or more of the above polypeptides, relative to a predetermined cut-off value. As used herein, suitable "biological samples" include blood, sera, urine and/or prostate secretions.

The level of one or more of the above polypeptides may be evaluated using any binding agent specific for the polypeptide(s). A "binding agent," in the context of this invention, is any agent (such as a compound or a cell) that binds to a polypeptide as described above. As used herein, "binding" refers to a noncovalent association between two separate molecules (each of which may be free (*i.e.*, in solution) or present on the surface of a cell or a solid support), such that a "complex" is formed. Such a complex may be free or immobilized (either covalently or noncovalently) on a support material. The ability to bind may generally be evaluated by determining a binding constant for the formation of the complex. The binding constant is the value obtained when the concentration of the complex is divided by the product of the component concentrations. In general, two compounds are said to "bind" in the context of the present invention when the binding constant for complex formation exceeds about 10^3 L/mol. The binding constant may be determined using methods well known to those of ordinary skill in the art.

Any agent that satisfies the above requirements may be a binding agent. For example, a binding agent may be a ribosome with or without a peptide component, an RNA molecule or a peptide. In a preferred embodiment, the binding partner is an antibody, or a fragment thereof. Such antibodies may be polyclonal, or monoclonal. In addition, the antibodies may be single chain, chimeric, CDR-grafted or humanized. Antibodies may be prepared by the methods described herein and by other methods well known to those of skill in the art.

There are a variety of assay formats known to those of ordinary skill in the art for using a binding partner to detect polypeptide markers in a sample. See, e.g., Harlow and Lane, *Antibodies: A Laboratory Manual*, Cold Spring Harbor Laboratory, 1988. In a preferred embodiment, the assay involves the use of binding partner immobilized on a solid support to bind to and remove the polypeptide from the remainder of the sample. The bound polypeptide may then be detected using a second binding partner that contains a reporter group. Suitable second binding partners include antibodies that bind to the binding partner/polypeptide complex. Alternatively, a competitive assay may be utilized, in which a

polypeptide is labeled with a reporter group and allowed to bind to the immobilized binding partner after incubation of the binding partner with the sample. The extent to which components of the sample inhibit the binding of the labeled polypeptide to the binding partner is indicative of the reactivity of the sample with the immobilized binding partner.

The solid support may be any material known to those of ordinary skill in the art to which the antigen may be attached. For example, the solid support may be a test well in a microtiter plate or a nitrocellulose or other suitable membrane. Alternatively, the support may be a bead or disc, such as glass, fiberglass, latex or a plastic material such as polystyrene or polyvinylchloride. The support may also be a magnetic particle or a fiber optic sensor, such as those disclosed, for example, in U.S. Patent No. 5,359,681. The binding agent may be immobilized on the solid support using a variety of techniques known to those of skill in the art, which are amply described in the patent and scientific literature. In the context of the present invention, the term "immobilization" refers to both noncovalent association, such as adsorption, and covalent attachment (which may be a direct linkage between the antigen and functional groups on the support or may be a linkage by way of a cross-linking agent). Immobilization by adsorption to a well in a microtiter plate or to a membrane is preferred. In such cases, adsorption may be achieved by contacting the binding agent, in a suitable buffer, with the solid support for a suitable amount of time. The contact time varies with temperature, but is typically between about 1 hour and about 1 day. In general, contacting a well of a plastic microtiter plate (such as polystyrene or polyvinylchloride) with an amount of binding agent ranging from about 10 ng to about 10 µg, and preferably about 100 ng to about 1 µg, is sufficient to immobilize an adequate amount of binding agent.

Covalent attachment of binding agent to a solid support may generally be achieved by first reacting the support with a bifunctional reagent that will react with both the support and a functional group, such as a hydroxyl or amino group, on the binding agent. For example, the binding agent may be covalently attached to supports having an appropriate polymer coating using benzoquinone or by condensation of an aldehyde group on the support with an amine and an active hydrogen on the binding partner (see, e.g., Pierce Immunotechnology Catalog and Handbook, 1991, at A12-A13).

In certain embodiments, the assay is a two-antibody sandwich assay. This assay may be performed by first contacting an antibody that has been immobilized on a solid support, commonly the well of a microtiter plate, with the sample, such that polypeptides within the sample are allowed to bind to the immobilized antibody. Unbound sample is then removed from the immobilized polypeptide-antibody complexes and a second antibody (containing a reporter group) capable of binding to a different site on the polypeptide is added. The amount of second antibody that remains bound to the solid support is then determined using a method appropriate for the specific reporter group.

More specifically, once the antibody is immobilized on the support as described above, the remaining protein binding sites on the support are typically blocked. Any suitable blocking agent known to those of ordinary skill in the art, such as bovine serum albumin or Tween 20TM (Sigma Chemical Co., St. Louis, MO). The immobilized antibody is then incubated with the sample, and polypeptide is allowed to bind to the antibody. The sample may be diluted with a suitable diluent, such as phosphate-buffered saline (PBS) prior to incubation. In general, an appropriate contact time (*i.e.*, incubation time) is that period of time that is sufficient to detect the presence of polypeptide within a sample obtained from an individual with prostate cancer. Preferably, the contact time is sufficient to achieve a level of binding that is at least about 95% of that achieved at equilibrium between bound and unbound polypeptide. Those of ordinary skill in the art will recognize that the time necessary to achieve equilibrium may be readily determined by assaying the level of binding that occurs over a period of time. At room temperature, an incubation time of about 30 minutes is generally sufficient.

Unbound sample may then be removed by washing the solid support with an appropriate buffer, such as PBS containing 0.1% Tween 20TM. The second antibody, which contains a reporter group, may then be added to the solid support. Preferred reporter groups include enzymes (such as horseradish peroxidase), substrates, cofactors, inhibitors, dyes, radionuclides, luminescent groups, fluorescent groups and biotin. The conjugation of antibody to reporter group may be achieved using standard methods known to those of ordinary skill in the art.

The second antibody is then incubated with the immobilized antibody-polypeptide complex for an amount of time sufficient to detect the bound polypeptide. An appropriate amount of time may generally be determined by assaying the level of binding that occurs over a period of time. Unbound second antibody is then removed and bound second antibody is detected using the reporter group. The method employed for detecting the reporter group depends upon the nature of the reporter group. For radioactive groups, scintillation counting or autoradiographic methods are generally appropriate. Spectroscopic methods may be used to detect dyes, luminescent groups and fluorescent groups. Biotin may be detected using avidin, coupled to a different reporter group (commonly a radioactive or fluorescent group or an enzyme). Enzyme reporter groups may generally be detected by the addition of substrate (generally for a specific period of time), followed by spectroscopic or other analysis of the reaction products.

To determine the presence or absence of prostate cancer, the signal detected from the reporter group that remains bound to the solid support is generally compared to a signal that corresponds to a predetermined cut-off value. In one preferred embodiment, the cut-off value is the average mean signal obtained when the immobilized antibody is incubated with samples from patients without prostate cancer. In general, a sample generating a signal that is three standard deviations above the predetermined cut-off value is considered positive for prostate cancer. In an alternate preferred embodiment, the cut-off value is determined using a Receiver Operator Curve, according to the method of Sackett et al., *Clinical Epidemiology: A Basic Science for Clinical Medicine*, Little Brown and Co., 1985, p. 106-7. Briefly, in this embodiment, the cut-off value may be determined from a plot of pairs of true positive rates (*i.e.*, sensitivity) and false-positive rates (100%-specificity) that correspond to each possible cut-off value for the diagnostic test result. The cut-off value on the plot that is the closest to the upper left-hand corner (*i.e.*, the value that encloses the largest area) is the most accurate cut-off value; and a sample generating a signal that is higher than the cut-off value determined by this method may be considered positive. Alternatively, the cut-off value may be shifted to the left along the plot, to minimize the false positive rate, or to the right, to minimize the false negative rate. In general, a sample generating a signal that is higher than the cut-off value determined by this method is considered positive for prostate cancer.

In a related embodiment, the assay is performed in a flow-through or strip test format, wherein the antibody is immobilized on a membrane, such as nitrocellulose. In the flow-through test, polypeptides within the sample bind to the immobilized antibody as the sample passes through the membrane. A second, labeled antibody then binds to the antibody-polypeptide complex, as a solution containing the second antibody flows through the membrane. The detection of bound second antibody may then be performed as described above. In the strip test format, one end of the membrane to which antibody is bound is immersed in a solution containing the sample. The sample migrates along the membrane through a region containing second antibody and to the area of immobilized antibody. Concentration of second antibody at the area of immobilized antibody indicates the presence of prostate cancer. Typically, the concentration of second antibody at that site generates a pattern, such as a line, that can be read visually. The absence of such a pattern indicates a negative result. In general, the amount of antibody immobilized on the membrane is selected to generate a visually discernible pattern when the biological sample contains a level of polypeptide that would be sufficient to generate a positive signal in the two-antibody sandwich assay, in the format discussed above. Preferably, the amount of antibody immobilized on the membrane ranges from about 25 ng to about 1 μ g, and more preferably from about 50 ng to about 500 ng. Such tests can typically be performed with a very small amount of biological sample.

Of course, numerous other assay protocols exist that are suitable for use with the antigens or antibodies of the present invention. The above descriptions are intended to be exemplary only.

In another embodiment, the above polypeptides may be used as markers for the progression of prostate cancer. In this embodiment, assays as described above for the diagnosis of prostate cancer may be performed over time, and the change in the level of reactive polypeptide(s) evaluated. For example, the assays may be performed every 24-72 hours for a period of 6 months to 1 year, and thereafter performed as needed. In general, prostate cancer is progressing in those patients in whom the level of polypeptide detected by the binding agent increases over time. In contrast, prostate cancer is not progressing when the level of reactive polypeptide either remains constant or decreases with time.

Antibodies for use in the above methods may be prepared by any of a variety of techniques known to those of ordinary skill in the art. See, e.g., Harlow and Lane, *Antibodies: A Laboratory Manual*, Cold Spring Harbor Laboratory, 1988. In one such technique, an immunogen comprising the antigenic polypeptide is initially injected into any of a wide variety of mammals (e.g., mice, rats, rabbits, sheep and goats). In this step, the polypeptides of this invention may serve as the immunogen without modification. Alternatively, particularly for relatively short polypeptides, a superior immune response may be elicited if the polypeptide is joined to a carrier protein, such as bovine serum albumin or keyhole limpet hemocyanin. The immunogen is injected into the animal host, preferably according to a predetermined schedule incorporating one or more booster immunizations, and the animals are bled periodically. Polyclonal antibodies specific for the polypeptide may then be purified from such antisera by, for example, affinity chromatography using the polypeptide coupled to a suitable solid support.

Monoclonal antibodies specific for the antigenic polypeptide of interest may be prepared, for example, using the technique of Kohler and Milstein, *Eur. J. Immunol.* 6:511-519, 1976, and improvements thereto. Briefly, these methods involve the preparation of immortal cell lines capable of producing antibodies having the desired specificity (i.e., reactivity with the polypeptide of interest). Such cell lines may be produced, for example, from spleen cells obtained from an animal immunized as described above. The spleen cells are then immortalized by, for example, fusion with a myeloma cell fusion partner, preferably one that is syngeneic with the immunized animal. A variety of fusion techniques may be employed. For example, the spleen cells and myeloma cells may be combined with a nonionic detergent for a few minutes and then plated at low density on a selective medium that supports the growth of hybrid cells, but not myeloma cells. A preferred selection technique uses HAT (hypoxanthine, aminopterin, thymidine) selection. After a sufficient time, usually about 1 to 2 weeks, colonies of hybrids are observed. Single colonies are selected and tested for binding activity against the polypeptide. Hybridomas having high reactivity and specificity are preferred.

Monoclonal antibodies may be isolated from the supernatants of growing hybridoma colonies. In addition, various techniques may be employed to enhance the yield,

such as injection of the hybridoma cell line into the peritoneal cavity of a suitable vertebrate host, such as a mouse. Monoclonal antibodies may then be harvested from the ascites fluid or the blood. Contaminants may be removed from the antibodies by conventional techniques, such as chromatography, gel filtration, precipitation, and extraction. The polypeptides of this invention may be used in the purification process in, for example, an affinity chromatography step.

Monoclonal antibodies of the present invention may also be used as therapeutic reagents, to diminish or eliminate prostate tumors. The antibodies may be used on their own (for instance, to inhibit metastases) or coupled to one or more therapeutic agents. Suitable agents in this regard include radionuclides, differentiation inducers, drugs, toxins, and derivatives thereof. Preferred radionuclides include ⁹⁰Y, ¹²³I, ¹²⁵I, ¹³¹I, ¹⁸⁶Re, ¹⁸⁸Re, ²¹¹At, and ²¹²Bi. Preferred drugs include methotrexate, and pyrimidine and purine analogs. Preferred differentiation inducers include phorbol esters and butyric acid. Preferred toxins include ricin, abrin, diphtheria toxin, cholera toxin, gelonin, Pseudomonas exotoxin, Shigella toxin, and pokeweed antiviral protein.

A therapeutic agent may be coupled (e.g., covalently bonded) to a suitable monoclonal antibody either directly or indirectly (e.g., via a linker group). A direct reaction between an agent and an antibody is possible when each possesses a substituent capable of reacting with the other. For example, a nucleophilic group, such as an amino or sulphydryl group, on one may be capable of reacting with a carbonyl-containing group, such as an anhydride or an acid halide, or with an alkyl group containing a good leaving group (e.g., a halide) on the other.

Alternatively, it may be desirable to couple a therapeutic agent and an antibody via a linker group. A linker group can function as a spacer to distance an antibody from an agent in order to avoid interference with binding capabilities. A linker group can also serve to increase the chemical reactivity of a substituent on an agent or an antibody, and thus increase the coupling efficiency. An increase in chemical reactivity may also facilitate the use of agents, or functional groups on agents, which otherwise would not be possible.

It will be evident to those skilled in the art that a variety of bifunctional or polyfunctional reagents, both homo- and hetero-functional (such as those described in the

catalog of the Pierce Chemical Co., Rockford, IL), may be employed as the linker group. Coupling may be effected, for example, through amino groups, carboxyl groups, sulfhydryl groups or oxidized carbohydrate residues. There are numerous references describing such methodology, e.g., U.S. Patent No. 4,671,958, to Rodwell et al.

Where a therapeutic agent is more potent when free from the antibody portion of the immunoconjugates of the present invention, it may be desirable to use a linker group which is cleavable during or upon internalization into a cell. A number of different cleavable linker groups have been described. The mechanisms for the intracellular release of an agent from these linker groups include cleavage by reduction of a disulfide bond (e.g., U.S. Patent No. 4,489,710, to Spitzer), by irradiation of a photolabile bond (e.g., U.S. Patent No. 4,625,014, to Senter et al.), by hydrolysis of derivatized amino acid side chains (e.g., U.S. Patent No. 4,638,045, to Kohn et al.), by serum complement-mediated hydrolysis (e.g., U.S. Patent No. 4,671,958, to Rodwell et al.), and acid-catalyzed hydrolysis (e.g., U.S. Patent No. 4,569,789, to Blattler et al.).

It may be desirable to couple more than one agent to an antibody. In one embodiment, multiple molecules of an agent are coupled to one antibody molecule. In another embodiment, more than one type of agent may be coupled to one antibody. Regardless of the particular embodiment, immunoconjugates with more than one agent may be prepared in a variety of ways. For example, more than one agent may be coupled directly to an antibody molecule; or linkers which provide multiple sites for attachment can be used. Alternatively, a carrier can be used.

A carrier may bear the agents in a variety of ways, including covalent bonding either directly or via a linker group. Suitable carriers include proteins such as albumins (e.g., U.S. Patent No. 4,507,234, to Kato et al.), peptides and polysaccharides such as aminodextran (e.g., U.S. Patent No. 4,699,784, to Shih et al.). A carrier may also bear an agent by noncovalent bonding or by encapsulation, such as within a liposome vesicle (e.g., U.S. Patent Nos. 4,429,008 and 4,873,088). Carriers specific for radionuclide agents include radiohalogenated small molecules and chelating compounds. For example, U.S. Patent No. 4,735,792 discloses representative radiohalogenated small molecules and their synthesis. A radionuclide chelate may be formed from chelating compounds that include those containing

nitrogen and sulfur atoms as the donor atoms for binding the metal, or metal oxide, radionuclide. For example, U.S. Patent No. 4,673,562, to Davison et al. discloses representative chelating compounds and their synthesis.

A variety of routes of administration for the antibodies and immunoconjugates may be used. Typically, administration will be intravenous, intramuscular, subcutaneous or in the bed of a resected tumor. It will be evident that the precise dose of the antibody/immunoconjugate will vary depending upon the antibody used, the antigen density on the tumor, and the rate of clearance of the antibody.

Diagnostic reagents of the present invention may also comprise DNA sequences encoding one or more of the above polypeptides, or one or more portions thereof. For example, at least two oligonucleotide primers may be employed in a polymerase chain reaction (PCR) based assay to amplify prostate tumor-specific cDNA derived from a biological sample, wherein at least one of the oligonucleotide primers is specific for a DNA molecule encoding a prostate tumor protein of the present invention. The presence of the amplified cDNA is then detected using techniques well known in the art, such as gel electrophoresis. Similarly, oligonucleotide probes specific for a DNA molecule encoding a prostate tumor protein of the present invention may be used in a hybridization assay to detect the presence of an inventive polypeptide in a biological sample.

As used herein, the term "oligonucleotide primer/probe specific for a DNA molecule" means an oligonucleotide sequence that has at least about 80%, preferably at least about 90% and more preferably at least about 95%, identity to the DNA molecule in question. Oligonucleotide primers and/or probes which may be usefully employed in the inventive diagnostic methods preferably have at least about 10-40 nucleotides. In a preferred embodiment, the oligonucleotide primers comprise at least about 10 contiguous nucleotides of a DNA molecule having a sequence selected from SEQ ID Nos: 1-107, 109-111, 115-171, 173-175, 177 and 179-224. Preferably, oligonucleotide probes for use in the inventive diagnostic methods comprise at least about 15 contiguous oligonucleotides of a DNA molecule having a sequence provided in SEQ ID Nos: 1-107, 109-111, 115-171, 173-175, 177 and 179-224. Techniques for both PCR based assays and hybridization assays are well known in the art (see, for example, Mullis et al. *Ibid*; Ehrlich, *Ibid*). Primers or probes may

thus be used to detect prostate tumor-specific sequences in biological samples, including blood, semen, prostate tissue and/or prostate tumor tissue.

Polypeptides of the present invention that comprise an immunogenic portion of a prostate tumor protein may also be used for immunotherapy of prostate cancer, wherein the polypeptide stimulates the patient's own immune response to prostate tumor cells. In further aspects, the present invention provides methods for using one or more of the immunoreactive polypeptides encoded by a DNA molecule having a sequence provided in SEQ ID NO: 1-107, 109-111, 115-171, 173-175, 177 and 179-224 (or DNA encoding such polypeptides) for immunotherapy of prostate cancer in a patient. As used herein, a "patient" refers to any warm-blooded animal, preferably a human. A patient may be afflicted with a disease, or may be free of detectable disease. Accordingly, the above immunoreactive polypeptides may be used to treat prostate cancer or to inhibit the development of prostate cancer. The polypeptides may be administered either prior to or following surgical removal of primary tumors and/or treatment by administration of radiotherapy and conventional chemotherapeutic drugs.

In these aspects, the polypeptide is generally present within a pharmaceutical composition and/or a vaccine. Pharmaceutical compositions may comprise one or more polypeptides, each of which may contain one or more of the above sequences (or variants thereof), and a physiologically acceptable carrier. The vaccines may comprise one or more of such polypeptides and a non-specific immune response enhancer, such as an adjuvant, biodegradable microsphere (e.g., polylactic-glyactide) or a liposome (into which the polypeptide is incorporated). Pharmaceutical compositions and vaccines may also contain other epitopes of prostate tumor antigens, either incorporated into a combination polypeptide (i.e., a single polypeptide that contains multiple epitopes) or present within a separate polypeptide.

Alternatively, a pharmaceutical composition or vaccine may contain DNA encoding one or more of the above polypeptides, such that the polypeptide is generated *in situ*. In such pharmaceutical compositions and vaccines, the DNA may be present within any of a variety of delivery systems known to those of ordinary skill in the art, including nucleic acid expression systems, bacteria and viral expression systems. Appropriate nucleic acid

expression systems contain the necessary DNA sequences for expression in the patient (such as a suitable promoter). Bacterial delivery systems involve the administration of a bacterium (such as *Bacillus-Calmette-Guerrin*) that expresses an epitope of a prostate cell antigen on its cell surface. In a preferred embodiment, the DNA may be introduced using a viral expression system (e.g., vaccinia or other pox virus, retrovirus, or adenovirus), which may involve the use of a non-pathogenic (defective), replication competent virus. Suitable systems are disclosed, for example, in Fisher-Hoch et al., *PNAS* 86:317-321, 1989; Flexner et al., *Ann. N.Y. Acad. Sci.* 569:86-103, 1989; Flexner et al., *Vaccine* 8:17-21, 1990; U.S. Patent Nos. 4,603,112, 4,769,330, and 5,017,487; WO 89/01973; U.S. Patent No. 4,777,127; GB 2,200,651; EP 0,345,242; WO 91/02805; Berkner; *Biotechniques* 6:616-627, 1988; Rosenfeld et al., *Science* 252:431-434, 1991; Kolls et al., *PNAS* 91:215-219, 1994; Kass-Eisler et al., *PNAS* 90:11498-11502, 1993; Guzman et al., *Circulation* 88:2838-2848, 1993; and Guzman et al., *Cir. Res.* 73:1202-1207, 1993. Techniques for incorporating DNA into such expression systems are well known to those of ordinary skill in the art. The DNA may also be "naked," as described, for example, in published PCT application WO 90/11092, and Ulmer et al., *Science* 259:1745-1749, 1993, reviewed by Cohen, *Science* 259:1691-1692, 1993. The uptake of naked DNA may be increased by coating the DNA onto biodegradable beads, which are efficiently transported into the cells.

Routes and frequency of administration, as well as dosage, will vary from individual to individual and may parallel those currently being used in immunotherapy of other diseases. In general, the pharmaceutical compositions and vaccines may be administered by injection (e.g., intracutaneous, intramuscular, intravenous or subcutaneous), intranasally (e.g., by aspiration) or orally. Between 1 and 10 doses may be administered over a 3-24 week period. Preferably, 4 doses are administered, at an interval of 3 months, and booster administrations may be given periodically thereafter. Alternate protocols may be appropriate for individual patients. A suitable dose is an amount of polypeptide or DNA that is effective to raise an immune response (cellular and/or humoral) against prostate tumor cells in a treated patient. A suitable immune response is at least 10-50% above the basal (i.e., untreated) level. In general, the amount of polypeptide present in a dose (or produced *in-situ* by the DNA in a dose) ranges from about 1 pg to about 100 mg per kg of host, typically from

about 10 pg to about 1 mg, and preferably from about 100 pg to about 1 μ g. Suitable dose sizes will vary with the size of the patient, but will typically range from about 0.01 mL to about 5 mL.

While any suitable carrier known to those of ordinary skill in the art may be employed in the pharmaceutical compositions of this invention, the type of carrier will vary depending on the mode of administration. For "parenteral" administration, such as subcutaneous injection, the carrier preferably comprises water, saline, alcohol, a lipid, a wax and/or a buffer. For oral administration, any of the above carriers or a solid carrier, such as mannitol, lactose, starch, magnesium stearate, sodium saccharine, talcum, cellulose, glucose, sucrose, and/or magnesium carbonate, may be employed. Biodegradable microspheres (e.g., polylactic glycolide) may also be employed as carriers for the pharmaceutical compositions of this invention. Suitable biodegradable microspheres are disclosed, for example, in U.S. Patent Nos. 4,897,268 and 5,075,109.

Any of a variety of non-specific immune response enhancers may be employed in the vaccines of this invention. For example, an adjuvant may be included. Most adjuvants contain a substance designed to protect the antigen from rapid catabolism, such as aluminum hydroxide or mineral oil, and a nonspecific stimulator of immune response, such as lipid A, *Bordetella pertussis* or *Mycobacterium tuberculosis*. Such adjuvants are commercially available as, for example, Freund's Incomplete Adjuvant and Complete Adjuvant (Difco Laboratories, Detroit, MI) and Merck Adjuvant 65 (Merck and Company, Inc., Rahway, NJ).

Polypeptides disclosed herein may also be employed in *ex vivo* treatment of prostate cancer. For example, cells of the immune system, such as T cells, may be isolated from the peripheral blood of a patient, using a commercially available cell separation system, such as CellPro Incorporated's (Bothell, WA) CEPRATETM system (see U.S. Patent No. 5,240,856; U.S. Patent No. 5,215,926; WO 89/06280; WO 91/16116 and WO 92/07243). The separated cells are stimulated with one or more of the immunoreactive polypeptides contained within a delivery vehicle, such as a microsphere, to provide antigen-specific T cells. The population of tumor antigen-specific T cells is then expanded using standard techniques and the cells are administered back to the patient.

The following Examples are offered by way of illustration and not by way of limitation.

EXAMPLES

EXAMPLE 1

ISOLATION AND CHARACTERIZATION OF PROSTATE TUMOR POLYPEPTIDES

This Example describes the isolation of prostate tumor polypeptides from a prostate tumor cDNA library.

A human prostate tumor cDNA expression library was constructed from prostate tumor poly A⁺ RNA using a Superscript Plasmid System for cDNA Synthesis and Plasmid Cloning kit (BRL Life Technologies, Gaithersburg, MD 20897) following the manufacturer's protocol. Specifically, prostate tumor tissues were homogenized with polytron (Kinematica, Switzerland) and total RNA was extracted using Trizol reagent (BRL Life Technologies) as directed by the manufacturer. The poly A⁺ RNA was then purified using a Qiagen oligotex spin column mRNA purification kit (Qiagen, Santa Clarita, CA 91355) according to the manufacturer's protocol. First-strand cDNA was synthesized using the NotI/Oligo-dT18 primer. Double-stranded cDNA was synthesized, ligated with EcoRI/BAXI adaptors (Invitrogen, San Diego, CA) and digested with NotI. Following size fractionation with Chroma Spin-1000 columns (Clontech, Palo Alto, CA 94303), the cDNA was ligated into the EcoRI/NotI site of pCDNA3.1 (Invitrogen) and transformed into ElectroMax *E. coli* DH10B cells (BRL Life Technologies) by electroporation.

Using the same procedure, a normal human pancreas cDNA expression library was prepared from a pool of six tissue specimens (Clontech). The cDNA libraries were characterized by determining the number of independent colonies, the percentage of clones that carried insert, the average insert size and by sequence analysis. The prostate tumor library contained 1.64×10^7 independent colonies, with 70% of clones having an insert and the average insert size being 1745 base pairs. The normal pancreas cDNA library contained 3.3×10^6 independent colonies, with 69% of clones having inserts and the average insert size

being 1120 base pairs. For both libraries, sequence analysis showed that the majority of clones had a full length cDNA sequence and were synthesized from mRNA, with minimal rRNA and mitochondrial DNA contamination.

cDNA library subtraction was performed using the above prostate tumor and normal pancreas cDNA libraries, as described by Hara et al. (*Blood*, 84:189-199, 1994) with some modifications. Specifically, a prostate tumor-specific subtracted cDNA library was generated as follows. Normal pancreas cDNA library (70 µg) was digested with EcoRI, NotI, and SfuI, followed by a filling-in reaction with DNA polymerase Klenow fragment. After phenol-chloroform extraction and ethanol precipitation, the DNA was dissolved in 100 µl of H₂O, heat-denatured and mixed with 100 µl (100 µg) of Photoprobe biotin (Vector Laboratories, Burlingame, CA). As recommended by the manufacturer, the resulting mixture was irradiated with a 270 W sunlamp on ice for 20 minutes. Additional Photoprobe biotin (50 µl) was added and the biotinylation reaction was repeated. After extraction with butanol five times, the DNA was ethanol-precipitated and dissolved in 23 µl H₂O to form the driver DNA.

To form the tracer DNA, 10 µg prostate tumor cDNA library was digested with BamHI and XhoI, phenol chloroform extracted and passed through Chroma spin-400 columns (Clontech). Following ethanol precipitation, the tracer DNA was dissolved in 5 µl H₂O. Tracer DNA was mixed with 15 µl driver DNA and 20 µl of 2 x hybridization buffer (1.5 M NaCl/10 mM EDTA/50 mM HEPES pH 7.5/0.2% sodium dodecyl sulfate), overlaid with mineral oil, and heat-denatured completely. The sample was immediately transferred into a 68 °C water bath and incubated for 20 hours (long hybridization [LH]). The reaction mixture was then subjected to a streptavidin treatment followed by phenol/chloroform extraction. This process was repeated three more times. Subtracted DNA was precipitated, dissolved in 12 µl H₂O, mixed with 8 µl driver DNA and 20 µl of 2 x hybridization buffer, and subjected to a hybridization at 68 °C for 2 hours (short hybridization [SH]). After removal of biotinylated double-stranded DNA, subtracted cDNA was ligated into BamHI/XhoI site of chloramphenicol resistant pBCSK⁺ (Stratagene, La Jolla, CA 92037) and transformed into ElectroMax *E. coli* DH10B cells by electroporation to generate a prostate tumor specific subtracted cDNA library(prostate subtraction 1).

To analyze the subtracted cDNA library, plasmid DNA was prepared from 100 independent clones, randomly picked from the subtracted prostate tumor specific library and grouped based on insert size. Representative cDNA clones were further characterized by DNA sequencing with a Perkin Elmer/Applied Biosystems Division Automated Sequencer Model 373A (Foster City, CA). Six cDNA clones, hereinafter referred to as F1-13, F1-12, F1-16, H1-1, H1-9 and H1-4, were shown to be abundant in the subtracted prostate-specific cDNA library. The determined 3' and 5' cDNA sequences for F1-12 are provided in SEQ ID NO: 2 and 3, respectively, with determined 3' cDNA sequences for F1-13, F1-16, H1-1, H1-9 and H1-4 being provided in SEQ ID No: 1 and 4-7, respectively.

The cDNA sequences for the isolated clones were compared to known sequences in the gene bank using the EMBL and GenBank databases (release 96). Four of the prostate tumor cDNA clones, F1-13, F1-16, H1-1, and H1-4, were determined to encode the following previously identified proteins: prostate specific antigen (PSA), human glandular kallikrein, human tumor expression enhanced gene, and mitochondria cytochrome C oxidase subunit II. H1-9 was found to be identical to a previously identified human autonomously replicating sequence. No significant homologies to the cDNA sequence for F1-12 were found.

Subsequent studies led to the isolation of a full-length cDNA sequence for F1-12. This sequence is provided in SEQ ID NO: 107, with the corresponding predicted amino acid sequence being provided in SEQ ID NO: 108.

To clone less abundant prostate tumor specific genes, cDNA library subtraction was performed by subtracting the prostate tumor cDNA library described above with the normal pancreas cDNA library and with the three most abundant genes in the previously subtracted prostate tumor specific cDNA library: human glandular kallikrein, prostate specific antigen (PSA), and mitochondria cytochrome C oxidase subunit II. Specifically, 1 µg each of human glandular kallikrein, PSA and mitochondria cytochrome C oxidase subunit II cDNAs in pCDNA3.1 were added to the driver DNA and subtraction was performed as described above to provide a second subtracted cDNA library hereinafter referred to as the "subtracted prostate tumor specific cDNA library with spike".

Twenty-two cDNA clones were isolated from the subtracted prostate tumor specific cDNA library with spike. The determined 3' and 5' cDNA sequences for the clones referred to as J1-17, L1-12, N1-1862, J1-13, J1-19, J1-25; J1-24, K1-58, K1-63, L1-4 and L1-14 are provided in SEQ ID Nos: 8-9, 10-11, 12-13, 14-15, 16-17, 18-19, 20-21, 22-23, 24-25, 26-27 and 28-29, respectively. The determined 3' cDNA sequences for the clones referred to as J1-12, J1-16, J1-21, K1-48, K1-55, L1-2, L1-6, N1-1858, N1-1860, N1-1861, N1-1864 are provided in SEQ ID Nos: 30-40, respectively. Comparison of these sequences with those in the gene bank as described above, revealed no significant homologies to three of the five most abundant DNA species (J1-17, L1-12 and N1-1862; SEQ ID Nos: 8-9, 10-11 and 12-13, respectively). Of the remaining two most abundant species, one (J1-12; SEQ ID NO:30) was found to be identical to the previously identified human pulmonary surfactant-associated protein, and the other (K1-48; SEQ ID NO:33) was determined to have some homology to *R. norvegicus* mRNA for 2-arylpropionyl-CoA epimerase. Of the 17 less abundant cDNA clones isolated from the subtracted prostate tumor specific cDNA library with spike, four (J1-16, K1-55, L1-6 and N1-1864; SEQ ID Nos: 31, 34, 36 and 40, respectively) were found to be identical to previously identified sequences, two (J1-21 and N1-1860; SEQ ID Nos: 32 and 38, respectively) were found to show some homology to non-human sequences, and two (L1-2 and N1-1861; SEQ ID Nos: 35 and 39, respectively) were found to show some homology to known human sequences. No significant homologies were found to the polypeptides J1-13, J1-19, J1-24, J1-25, K1-58, K1-63, L1-4, L1-14 (SEQ ID Nos: 14-15, 16-17, 20-21, 18-19, 22-23, 24-25, 26-27, 28-29, respectively).

Subsequent studies led to the isolation of full length cDNA sequences for J1-17, L1-12 and N1-1862 (SEQ ID NOS: 109-111, respectively). The corresponding predicted amino acid sequences are provided in SEQ ID NOS: 112-114.

In a further experiment, four additional clones were identified by subtracting a prostate tumor cDNA library with normal prostate cDNA prepared from a pool of three normal prostate poly A+ RNA (prostate subtraction 2). The determined cDNA sequences for these clones, hereinafter referred to as U1-3064, U1-3065, V1-3692 and 1A-3905, are provided in SEQ ID NO: 69-72, respectively. Comparison of the determined sequences with those in the gene bank revealed no significant homologies to U1-3065.

A second subtraction with spike (prostate subtraction spike 2) was performed by subtracting a prostate tumor specific cDNA library with spike with normal pancreas cDNA library and further spiked with PSA; J1-17, pulmonary surfactant-associated protein, mitochondrial DNA, cytochrome c oxidase subunit II, N1-1862, autonomously replicating sequence, L1-12 and tumor expression enhanced gene. Four additional clones, hereinafter referred to as V1-3686, R1-2330, 1B-3976 and V1-3679, were isolated. The determined cDNA sequences for these clones are provided in SEQ ID NO:73-76, respectively. Comparison of these sequences with those in the gene bank revealed no significant homologies to V1-3686 and R1-2330.

Further analysis of the three prostate subtractions described above (prostate subtraction 2, subtracted prostate tumor specific cDNA library with spike; and prostate subtraction spike 2), resulted in the identification of sixteen additional clones, referred to as 1G-4736, 1G-4738, 1G-4741; 1G-4744, 1G-4734, 1H-4774, 1H-4781, 1H-4785, 1H-4787, 1H-4796, 1I-4810, 1I-4811, 1J-4876, 1K-4884 and 1K-4896. The determined cDNA sequences for these clones are provided in SEQ ID NOS: 77-92, respectively. Comparison of these sequences with those in the gene bank as described above, revealed no significant homologies to 1G-4741, 1G-4734, 1I-4807, 1J-4876 and 1K-4896 (SEQ ID NOS: 79, 81, 87, 90 and 92, respectively). Further analysis of the isolated clones led to the determination of extended cDNA sequences for 1G-4736, 1G-4738, 1G-4741, 1G-4744, 1H-4774, 1H-4781, 1H-4785, 1H-4787, 1H-4796, 1I-4807, 1J-4876, 1K-4884 and 1K-4896, provided in SEQ ID NOS: 179-188 and 191-193, respectively, and to the determination of additional partial cDNA sequences for 1I-4810 and 1I-4811, provided in SEQ ID NOS: 189 and 190, respectively.

An additional subtraction was performed by subtracting a normal prostate cDNA library with normal pancreas cDNA (prostate subtraction 3). This led to the identification of six additional clones referred to as 1G-4761, 1G-4762, 1H-4766, 1H-4770, 1H-4771 and 1H-4772 (SEQ ID NOS: 93-98). Comparison of these sequences with those in the gene bank revealed no significant homologies to 1G-4761 and 1H-4771 (SEQ ID NOS: 93 and 97, respectively). Further analysis of the isolated clones led to the determination of extended cDNA sequences for 1G-4761, 1G-4762, 1H-4766 and 1H-4772 provided in SEQ

ID NOS: 194-196 and 199, respectively; and to the determination of additional partial cDNA sequences for 1H-4770 and 1H-4771, provided in SEQ ID NOS: 197 and 198, respectively.

Subtraction of a prostate tumor cDNA library, prepared from a pool of polyA+ RNA from three prostate cancer patients, with a normal pancreas cDNA library (prostate subtraction 4) led to the identification of eight clones, referred to as 1D-4297, 1D-4309, 1D-4278, 1D-4288, 1D-4283, 1D-4304, 1D-4296 and 1D-4280 (SEQ ID NOS: 99-107). These sequences were compared to those in the gene bank as described above. No significant homologies were found to 1D-4283 and 1D-4304 (SEQ ID NOS: 103 and 104, respectively). Further analysis of the isolated clones led to the determination of extended cDNA sequences for 1D-4309, 1D-4278, 1D-4288, 1D-4283, 1D-4304, 1D-4296 and 1D-4280, provided in SEQ ID NOS: 200-206, respectively.

cDNA clones isolated in prostate subtraction 1 and prostate subtraction 2, described above, were colony PCR amplified and their mRNA expression levels in prostate tumor, normal prostate and in various other normal tissues were determined using microarray technology (Synteni, Palo Alto, CA). Briefly, the PCR amplification products were dotted onto slides in an array format, with each product occupying a unique location in the array. mRNA was extracted from the tissue sample to be tested, reverse transcribed, and fluorescent-labeled cDNA probes were generated. The microarrays were probed with the labeled cDNA probes, the slides scanned and fluorescence intensity was measured. This intensity correlates with the hybridization intensity. Two novel clones (referred to as P509S and P510S) were found to be over-expressed in prostate tumor and normal prostate and expressed at low levels in all other normal tissues tested (liver, pancreas, skin, bone marrow, brain, breast, adrenal gland, bladder, testes, salivary gland, large intestine, kidney, ovary, lung, spinal cord, skeletal muscle and colon). The determined cDNA sequences for P509S and P510S are provided in SEQ ID NO: 223 and 224, respectively. Comparison of these sequences with those in the gene bank as described above, revealed some homology to previously identified ESTs.

EXAMPLE 2
DETERMINATION OF TISSUE SPECIFICITY OF PROSTATE TUMOR POLYPEPTIDES

Using gene specific primers, mRNA expression levels for the representative prostate tumor polypeptides F1-16, H1-1, J1-17, L1-12; F1-12 and N1-1862 were examined in a variety of normal and tumor tissues using RT-PCR.

Briefly, total RNA was extracted from a variety of normal and tumor tissues using Trizol reagent as described above. First strand synthesis was carried out using 1-2 µg of total RNA with SuperScript II reverse transcriptase (BRL Life Technologies) at 42 °C for one hour. The cDNA was then amplified by PCR with gene-specific primers. To ensure the semi-quantitative nature of the RT-PCR, β-actin was used as an internal control for each of the tissues examined. First, serial dilutions of the first strand cDNAs were prepared and RT-PCR assays were performed using β-actin specific primers. A dilution was then chosen that enabled the linear range amplification of the β-actin template and which was sensitive enough to reflect the differences in the initial copy numbers. Using these conditions, the β-actin levels were determined for each reverse transcription reaction from each tissue. DNA contamination was minimized by DNase treatment and by assuring a negative PCR result when using first strand cDNA that was prepared without adding reverse transcriptase.

mRNA Expression levels were examined in four different types of tumor tissue (prostate tumor from 2 patients, breast tumor from 3 patients, colon tumor, lung tumor), and sixteen different normal tissues, including prostate, colon, kidney, liver, lung, ovary, pancreas, skeletal muscle, skin, stomach, testes, bone marrow and brain. F1-16 was found to be expressed at high levels in prostate tumor tissue, colon tumor and normal prostate, and at lower levels in normal liver, skin and testes, with expression being undetectable in the other tissues examined. H1-1 was found to be expressed at high levels in prostate tumor, lung tumor, breast tumor, normal prostate, normal colon and normal brain; at much lower levels in normal lung, pancreas, skeletal muscle, skin, small intestine, bone marrow, and was not detected in the other tissues tested. J1-17 and L1-12 appear to be specifically over-expressed in prostate, with both genes being expressed at high levels in prostate tumor and normal prostate but at low to undetectable levels in all the other tissues

examined. N1-1862 was found to be over-expressed in 60% of prostate tumors and detectable in normal colon and kidney. The RT-PCR results thus indicate that F1-16, H1-1, J1-17, N1-1862 and L1-12 are either prostate specific or are expressed at significantly elevated levels in prostate.

Further RT-PCR studies showed that F1-12 is over-expressed in 60% of prostate tumors, detectable in normal kidney but not detectable in all other tissues tested. Similarly, R1-2330 was shown to be over-expressed in 40% of prostate tumors, detectable in normal kidney and liver, but not detectable in all other tissues tested. U1-3064 was found to be over-expressed in 60% of prostate tumors, and also expressed in breast and colon tumors, but was not detectable in normal tissues. RT-PCR characterization of R1-2330, U1-3064 and 1D-4279 showed that these three antigens are over-expressed in prostate and/or prostate tumors.

Northern analysis with four prostate tumors, two normal prostate samples, two BPH prostates, and normal colon, kidney, liver, lung, pancreas, skeletal muscle, brain, stomach, testes, small intestine and bone marrow, showed that L1-12 is over-expressed in prostate tumors and normal prostate, while being undetectable in other normal tissues tested. J1-17 was detected in two prostate tumors and not in the other tissues tested. N1-1862 was found to be over-expressed in three prostate tumors and to be expressed in normal prostate, colon and kidney, but not in other tissues tested. F1-12 was found to be highly expressed in two prostate tumors and to be undetectable in all other tissues tested.

The micro-array technology described above was used to determine the expression levels of representative antigens described herein in prostate tumor, breast tumor and the following normal tissues: prostate, liver, pancreas, skin, bone marrow, brain, breast, adrenal gland, bladder, testes, salivary gland, large intestine, kidney, ovary, lung, spinal cord, skeletal muscle and colon. L1-12 was found to be over-expressed in normal prostate and prostate tumor, with some expression being detected in normal skeletal muscle. Both J1-12 and F1-12 were found to be over-expressed in prostate tumor, with expression being lower or undetectable in all other tissues tested. N1-1862 was found to be expressed at high levels in prostate tumor and normal prostate, and at low levels in normal large intestine and normal colon, with expression being undetectable in all other tissues tested. R1-2330 was found to

be over-expressed in prostate tumor and normal prostate, and to be expressed at lower levels in all other tissues tested. 1D-4279, was found to be over-expressed in prostate tumor and normal prostate, expressed at lower levels in normal spinal cord, and to be undetectable in all other tissues tested.

Example 3

ISOLATION AND CHARACTERIZATION OF PROSTATE TUMOR POLYPEPTIDES BY PCR-BASED SUBTRACTION

A cDNA subtraction library, containing cDNA from normal prostate subtracted with ten other normal tissue cDNAs (brain, heart, kidney, liver, lung, ovary, placenta, skeletal muscle, spleen and thymus) and then submitted to a first round of PCR amplification, was purchased from Clontech. This library was subjected to a second round of PCR amplification, following the manufacturer's protocol. The resulting cDNA fragments were subcloned into the vector pT7 Blue T-vector (Novagen, Madison, WI) and transformed into XL-1 Blue MRF' *E. coli* (Stratagene). DNA was isolated from independent clones and sequenced using a Perkin Elmer/Applied Biosystems Division Automated Sequencer Model 373A.

Fifty-nine positive clones were sequenced. Comparison of the DNA sequences of these clones with those in the gene bank, as described above, revealed no significant homologies to 25 of these clones, hereinafter referred to as P5, P8, P9, P18, P20, P30, P34, P36, P38, P39, P42, P49, P50, P53, P55, P60, P64, P65, P73, P75, P76, P79, and P84. The determined cDNA sequences for these clones are provided in SEQ ID NO:41-45, 47-52 and 54-65, respectively. P29, P47, P68, P80 and P82 (SEQ ID NO:46, 53 and 66-68, respectively) were found to show some degree of homology to previously identified DNA sequences. To the best of the inventors' knowledge, none of these sequences have been previously shown to be present in prostate. Further studies using the PCR-based methodology described above resulted in the isolation of more than 180 additional clones, of which 23 clones were found to show no significant

homologies to known sequences. The determined cDNA sequences for these clones are provided in SEQ ID NO: 115, 123, 127, 131, 137, 145, 147-151, 153, 156-158 and 160. Twenty-three clones (SEQ ID NO: 124-126, 128-130, 132-136, 138-144, 146, 152, 154, 155 and 159) were found to show some homology to previously identified ESTs. An additional ten clones (SEQ ID NO: 161-170) were found to have some degree of homology to known genes. An additional clone, referred to as P703, was found to have five splice variants. The determined DNA sequence for the variants referred to as DE1, DE13 and DE14 are provided in SEQ ID NOS: 171, 175 and 177, respectively, with the corresponding predicted amino acid sequences being provided in SEQ ID NO: 172, 176 and 178, respectively. The DNA sequences for the splice variants referred to as DE2 and DE6 are provided in SEQ ID NOS: 173 and 174, respectively.

mRNA Expression levels for representative clones in tumor tissues (prostate (n=5), breast (n=2), colon and lung) normal tissues (prostate (n=5), colon, kidney, liver, lung (n=2), ovary (n=2), skeletal muscle, skin, stomach, small intestine and brain), and activated and non-activated PBMC was determined by RT-PCT as described above. Expression was examined in one sample of each tissue type unless otherwise indicated.

P9 was found to be highly expressed in normal prostate and prostate tumor compared to all normal tissues tested except for normal colon which showed comparable expression. P20 was found to be highly expressed in normal prostate and prostate tumor, compared to all twelve normal tissues tested. A modest increase in expression of P20 in breast tumor (n=2), colon tumor and lung tumor was seen compared to all normal tissues except lung (1 of 2). Increased expression of P18 was found in normal prostate, prostate tumor and breast tumor compared to other normal tissues except lung and stomach. A modest increase in expression of P5 was observed in normal prostate compared to most other normal tissues. However, some elevated expression was seen in normal lung and PBMC. Elevated expression of P5 was also observed in prostate tumors (2 of 5), breast tumor and one lung tumor sample. For P30, similar expression levels were seen in normal prostate and prostate tumor, compared to six of twelve other normal tissues tested. Increased expression was seen in breast tumors, one lung tumor sample and one colon tumor sample, and also in normal PBMC. P29 was found to be over-expressed in prostate tumor (5 of 5) and normal prostate (5

of 5) compared to the majority of normal tissues. However, substantial expression of P29 was observed in normal colon and normal lung (2 of 2). P80 was found to be over-expressed in prostate tumor (5 of 5) and normal prostate (5 of 5) compared to all other normal tissues tested, with increased expression also being seen in colon tumor.

Further studies using the above methodology resulted in the isolation of twelve additional clones, hereinafter referred to as 10-d8, 10-h10, 11-c8, 7-g6, 8-b5, 8-b6, 8-d4, 8-d9, 8-g3, 8-h11, g-f12 and g-f3. The determined DNA sequences for 10-d8, 10-h10, 11-c8, 8-d4, 8-d9, 8-h11, g-f12 and g-f3 are provided in SEQ ID NO: 207, 208, 209, 216, 217, 220, 221 and 222, respectively. The determined forward and reverse DNA sequences for 7-g6, 8-b5, 8-b6 and 8-g3 are provided in SEQ ID NO: 210 and 211; 212 and 213; 214 and 215; and 218 and 219, respectively. Comparison of these sequences with those in the gene bank revealed no significant homologies to the sequences of 7-g6 and g-f3. The clones 10-d8, 11-c8 and 8-h11 were found to show some homology to previously isolated ESTs, while 10-h10, 8-b5, 8-b6, 8-d4, 8-d9, 8-g3 and g-f12 were found to show some homology to previously identified genes.

EXAMPLE 4 SYNTHESIS OF POLYPEPTIDES

Polypeptides may be synthesized on an Applied Biosystems 430A peptide synthesizer using FMOC chemistry with HPTU (O-Benzotriazole-N,N,N',N"-tetramethyluronium hexafluorophosphate) activation. A Gly-Cys-Gly sequence may be attached to the amino terminus of the peptide to provide a method of conjugation, binding to an immobilized surface, or labeling of the peptide. Cleavage of the peptides from the solid support may be carried out using the following cleavage mixture: trifluoroacetic acid:ethanedithiol:thioanisole:water:phenol (40:1:2:2:3). After cleaving for 2 hours, the peptides may be precipitated in cold methyl-t-butyl-ether. The peptide pellets may then be dissolved in water containing 0.1% trifluoroacetic acid (TFA) and lyophilized prior to purification by C18 reverse phase HPLC. A gradient of 0%-60% acetonitrile (containing 0.1% TFA) in water (containing 0.1% TFA) may be used to elute the peptides. Following

lyophilization of the pure fractions, the peptides may be characterized using electrospray or other types of mass spectrometry and by amino acid analysis.

From the foregoing, it will be appreciated that, although specific embodiments of the invention have been described herein for the purposes of illustration, various modifications may be made without deviating from the spirit and scope of the invention.

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANTS: Xu, Jiangchun

Dillon, Davin C.

(ii) TITLE OF INVENTION: COMPOUNDS FOR IMMUNODIAGNOSIS OF PROSTATE CANCER
AND METHODS FOR THEIR USE

(iii) NUMBER OF SEQUENCES: 224

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: SEED and BERRY LLP
(B) STREET: 6300 Columbia Center, 701 Fifth Avenue
(C) CITY: Seattle
(D) STATE: WA
(E) COUNTRY: USA
(F) ZIP: 98104

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER:
(B) FILING DATE: 23-FEB-1998
(C) CLASSIFICATION:

(vii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Maki, David J.
(B) REGISTRATION NUMBER: 31,392
(C) REFERENCE/DOCKET NUMBER: 210121.428C3

(ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: (206) 622-4900
(B) TELEFAX: (206) 682-6031

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 814 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

TTTTTTTTT TTTTCACAG TATAACAGCT CTTTATTTCT GTGAGTTCTA CTAGGAAATC

ATCAAATCTG AGGGGTGCT GGAGGACTTC AATACACCTC CCCCCATAGT GAATCAGCTT
 CCAGGGGTC CAGCCCTCT CCTTAATCTA TCCCCATCCC ATGCCAAAGG AAGACCCCTCC
 CTCTTGCTC CACAGCCTTC TCTAGGCTTC CCAGTGCCTC CAGGACAGAC TGTTATGT
 TTTCAGCTTC ATCCTTGTCT TGAGTGTCTG GTGCGTTGTG CCTCCACCTT CTGCTCAGTG
 CTTCATGGAC AGTGTCCAGC ACATGTCACT CTCCACCTTC TCAGTGTGGA TCCACTAGTT
 CTAGAGCGGC CGCCACCCGG GTGAGGCTTC AGCTTTGTGTT CCCTTAGITG AGGGTTAATT
 GCGCGCTTGG CGTATCATG GTCATAACTG TTCTCTGTGTA AAATTTGTTA TCCGCTACA
 ATTCAACACA ACATACGAGC CGGAAGCATA AAGTGTAAAG CCTGGGGTGC CTAATGAGTG
 ANCTAACTCA CATTAAATGG GTTGCCTCA CTGNCCTT TCGAGTCNGG AAAATGTCG
 TGCCAGCTGC ATTAATGAAT CGGCCAACGC NCAGGGAAAAA CGGGTTGGG TTTTGGGGC
 TCTTCGGCT CTCGCTCACT NANTCTGCG CTGGCTNTT CGGCTGCGGG GAACGTTATC
 ACTCTCAA GGNGTATTAA CGGGTATCCN NAATCNGG GATAACCNGG AAAAANNTT
 AACAAAAGGG CANCAAAGGG CNGAAACGTA AAAA

120
180
240
300
360
420
480
540
600
660
720
780
814

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 816 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ_ID NO:2:

ACAGAAATGT TGGATGTTG AGCACCTTC TATACCGCTT ACAGGACAGC AGATGGGGAA
 TTTCATGGCTG TTGGAGCAAT AGAACCCCAAG TTCTACGAGC TGCTGATCAA AGGACTTGG
 CTAAAGCTG ATGAACTTC CAATCAGATG AGCATGGATG ATTGGCCAGA AATGAAGAAG
 AAGTTGAGC ATGATTTCG AAAGAAGACG AGGCCAGAGT OGTTCAAT CTTTGACGGC
 ACAGATGCT GTGTGACTCC GTTCTGACT TTGAGGAGG TGTTCTATCA TGATTCACAC
 AAGGAACCGG GCTCTGATC CACAGTGAG GAGCAGGAG TGAGCCCCC CCCCTGACCT
 CTGCTGTTAA ACACCCCAAG CATCCCTCT TTCAAAAGGC ATCCACTAGT TCTAGAAGGG
 GCGCCACCCG CGGTGAGCT CCAGCTTTG TTCCCTTAG TGAGGGTTAA TTGCGGGCTT
 GGCCTAATTCG TTGTCATAGC TTGTTTCTGT GTGAATTGT TATCCGCTCA CAAATCCCC
 AACATACGAG CGGGACACATA AAGTGTAAAG CCTGGGGTGC CTAATGANTG AGCTAACTCN
 CATTAAATGC GTTGCCTCA CTGGCCGTT CTCAGTGGG AAAACTGTG TGCCACTGCG
 TTATGAAATC NGGACCCCC CGGGAAAGG CGGGTTGNTT TTGGGCTCT TCCGGTTTC
 TCGCTCATTT ATCCCTNGCC CGGGTCTTCG GTGCGCNGA ACGGTTCACT CCTCAAAGGC
 GTGNTNCAGG TTATCCCCA ACNGGGATA CCCNGA

60
120
180
240
300
360
420
480
540
600
660
720
780
816

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 773 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ_ID NO:3:

CTTTTGAAAG AAGGGATGGC TGGGGTTT AACAGCAGAG GTGCAGGGCG GGGGCTCAGC
 TCTCTGCTCT CACTGGTGT AAACGAGCCC CGTTCTGT TGTGATCATG ATGAACAACC

60
120

TCCTCAAAAG	TCAGAACCGG	AGTCACACAG	GCATCTGTG	CGTCAAAGAT	TTGACACCAC	180
TCTGCCCTTC	TCTTCTTGG	AAATACATCT	GCAACTCT	TCTTCATTTC	TGGCCAAATCA	240
TCCATGCTCA	TCTGATGGG	AAAGTCATCA	GACTTTAGTC	CANNTCTTT	GATCAGCAGG	300
TCCTAGAAGT	GGGGTTCTAT	TGCTCCAAACA	GCCATGAAT	CCCCATCTGC	TGTCCTGTAA	360
GTCGTATAGA	AAGGTGCTCC	ACCATCCAC	ATGTTCTGTC	CTCGAGGGGG	GGCCCGGTAC	420
CCAATTCGGC	CTATANTGAG	TGTTTACAG	CGCGCTCACT	GGCGTGTGTT	TTACAACGTC	480
GTGACTGGGA	AAACCTGGG	CGTTACCAAA	TTAATCGCT	TGCAGCACAT	CCCCCTTTCG	540
CCAGCTGGGC	GTAAATANGA	AAAGGCCCGC	ACCGATGCC	CTTCCAAACAG	TTGCGCACCT	600
GAATGGNAA	ATGGGACCCC	CCTGTACCG	CGCATTAAC	CCCCGCNGG	TTTNGTGTGTT	660
ACCCCCACNT	NNACCCTTA	CACTTTCACCA	GGCCCTTANC	GCCCGCTCC	TTTCCTTCTT	720
CTTCCCTTC	TTTCNCNNCN	CTTTCCTCCG	GGGTTTCCCC	CNTCAAAACCC	CNA	773

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 828 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

CCTCTCTGAGT	CCTACTGAGT	TGTGCTTCT	GTTGTGGAGT	CCAGGGCTGC	TAGGAAAAGG	60
ATGGGGCGA	CACAGGTGTA	TGCCATGTT	TCTGAATGG	GTATAATTTC	GTCTCTCTCT	120
TCGGACACT	GGCTGTCTCT	GAAGACTCT	CGCTCAGTG	CAGTGGAGAC	ACACACAAAG	180
ACGCTGGTGA	CCATGTTGTT	TGTGGGGTGC	AGAGATGGGA	GGGGTGGGGC	CCACCTGGG	240
AGAGTGGACA	GTGACACACG	GTGACACTCT	TCTACAGATC	ACTGAGGATA	AGCTGGAGCC	300
ACAATCATG	AGGCACACAC	ACAGCAGGA	TGACNCTGTA	AACATAGCCC	ACGGTGTCTT	360
GNGGGCACGT	GAAGACCTG	ATNAGGGCTG	GAGCANAAGA	GGGGGAGGA	TCCACTAGTT	420
CTANACGGG	CGCCACCCGG	GTGANCTCC	ANCTTGTGTT	CCCTTGTAGT	AGGGTTAATT	480
GGCGCTTGG	CNTAATCATG	GTCTACATCT	TTCTCTGTG	GAATTTGTTA	TCCGCTCACA	540
ATTCACACAA	ACATACAGC	CGGAACATCA	AAATGTAAC	CTGGGGTGC	TAATGANTGA	600
CTAACCTACA	TTAATTGCT	TGGCCTACT	GCCCGCTTC	CAATCNGAA	ACCTCTCTTG	660
CCNCTTGAT	TNTAGATCTN	GGCAACCCCC	GGGGAAAAGC	GTTGGCTTT	TGGGGCTCT	720
TCCGGCTCC	CNTCTCTTA	NTCCCTNC	TGGTCTATC	CGGTGCGNC	AAACCGGTT	780
ACCNCCTCA	AAAGGGGTAT	TCCGGTTTC	CCNAATCCG	GGANANCC		828

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 834 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

TTTTTTTTT	TTTTTACTGAA	TAGATGGAAT	TTATTAAGCT	TTTCACATGT	GATAGCACAT	60
AGTTTTAAAT	GCATCCAAG	TACTAACAA	AACTCTAGCA	ATCAAGAATG	GCAGCATGTT	120
ATTTTATAAC	AATCAACACC	TGTGGCTTT	AAAATTTGGT	TTTCATAGA	TAATTTATAC	180
TGAGAATTAAT	CTAGCCATGC	TTTTAAAAAA	TGCTTTAGGT	CACTCCAAGC	TTGGCGATTA	240

ACATTTGGCA	TAACAAATAA	AAAAACAATC	ACAATTAAAT	AAATAACAAA	TACAACATTG	300
TAGGCCATAA	TCATATACAG	TATAAGGAAA	AGGTGGTAGT	GTTGAGTAAG	CAGTTATTAG	350
AATAGAACAT	CTTGGCCCTCT	ATGCAAATAT	GTCTAGACAC	TTTGATTCAAC	TCAGCCCCGA	420
CATTCACTT	TCAAAGTAGG	AGACAGGTTG	TACAGTATCA	TTTACAGTT	TCCAAGACAT	480
TGAAACAAAG	TAGAAAATGAA	TGACTGTGTT	TTTATTAAATG	CATTACATCC	TCAAGAGGTA	540
CTACCAACCC	CTCAGTTATA	AAAATTTTC	AACTTATATT	AGTCATATAA	CTTGGTGTGC	600
TTATTTAA	TTAGTGCTAA	ATGGATTAACG	TGAGAACAC	AATGGTCCCC	TAATGTGATT	660
GATATGGT	ATTTTACCA	GCTTCTTAAT	CTNAACTTTC	AGGGTTTGA	ACTGGACAT	720
TGNAATNACAG	TGTCACANAG	TTNACACTA	CTGGAACATT	ACAGTGTGCT	TGATTCAAAA	780
TTGTTTTTG	TTAAAAAATTA	AATTTTAAC	TGGTGGAAAA	ATAATTGAA	ATNA	834

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 818 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

TTTTTTTTT	TTTTTTTTT	AAAGACCTCA	TCAAATAGAT	GAGACATACA	GAAATAGTCA	60
AACCAACTCT	ACAAAATGCC	AGTATCAGGC	GGCGGCTTCG	AAGCCAAGT	GATGTTTGG	120
TGAAAGTGA	AATATTAGTT	GGCGGATGAA	GCAGATAGTG	AGGAAATGTT	AGCCAATAAT	180
GACGTGAAGT	CCGTGGAACTG	CTGTGCTCAC	AAAAATGTT	GAGCCGTTAGA	TGCGGTGCGGA	240
AATGTCGAAG	GGAGACTCGA	AGTACTCTGA	GGCTTGTAGG	AGGGTAAAT	AGAGACCCAG	300
TAAATTGTA	ATAAGCAGTG	CTTGTGTTAT	TGGTTTTCG	TTGTTTCTCA	TTAGACTATG	360
GTGAGCTCAG	GTGATGATCA	CTCTGTATGC	GAGTAATAGC	GATGTTGTTA	GGAGTGGGAC	420
TTCTAGGGG	TTTAGGGGGG	TGATGCCCTG	TGGGGGCCAG	TGCCCTCTCA	GTGTTGGGGT	480
AGGGGCTAGG	CTGGAGTGGT	AAAAGGCTCA	AAAAAATCTT	GCGAAGAAAA	AAACTCTGA	540
GGAATAATAAT	AGGGATTATCC	CGTATCGAAG	GCCTTTTTCG	ACAGGTGGT	TCTGGTGGCC	600
TTGGTAGTG	CTTCTTCGTC	TTACATCGCG	CCATCATTTG	TATATGTTA	GTGTGTTGG	660
TTTANTANGC	CTTANTATGAA	GAACCTTGG	ANTGGAATTA	AATCAATNGC	TTGGCCGGAA	720
GTCATTANGA	NGGCTNAAA	GGCCCTGTTA	NGGGCTGGG	CTNGTTTTA	CCCNACCCAT	780
GGAAATCNCC	CCCCGGACNA	NTGNATCCCT	ATTCTTAA			818

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 817 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

TTTTTTTTT	TTTTTTTTT	TGGCTCTAGA	GGGGCTAGAG	GGGGTCTAT	AGGGTAAATA	60
CGGGCCCTAT	TTCAAAAGATT	TTTGGGGAA	TTAATCTAG	GACGATGGGT	ATGAAACTGT	120
GTTTGTCTCC	ACAGATTCA	GAGCATGAC	CGTAGATATAC	CCCGCGTCGT	GTAGCGGTGA	180
AAGTGGTTG	TTTACAGCT	CCGGGAATTG	CATCTGTTT	TAAGCCTAAT	GTGGGGACAG	240
CTCATGAGT	CAAGACGCT	TGTGATGTA	TTATTATACN	AATGGGGCT	TCAATCGGGA	300

GTACTACTCG ATTGTCAAGC TCAAGGAGTC GCAGGGTGCCT CGGGTCTAGG AATAATGGGG 360
 GAAAGTATGTA GGAATTGAGA ATTAATCCG CGTAGTCGGT GTTCTCTAG GTTCAATACC 420
 ATTGGTGGCC AATTGATTG ATGGTAAGGG GAGGGATCGT TGAACCTCTC TGTTATGTA 480
 AGGATNCCTT NGGGATGGGA AGGCNATNAAG GGAACATANGGA TNAATGGGG GCANGATATT 540
 TCAAACNGTC TCTANTCTT GAAACGCTGTG AAATGTTAAT TAAATAAAN TTTNGTTATT 600
 GAATNTTNG GAAAAGGGT TACAGGACTA GAAACCCAAT ANGAAAANTA ATNNTAANGG 660
 CNTTATCNNTT AAAGGTNATA ACCNCTCCCTA TNATCCCACCC CAATNGNATT CCCCCACCN 720
 ACNATTGGAT NCCTTCANTT CANAANAGGC CNCCCCCCGG TGNANNCNC CTTTGTTC 780
 CTTNANTGAN GGTTTATTCCNC CCCTNGCNNTT ATCANCC 817

(2) INFORMATION FOR SEQ ID NO:8:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 799 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

CATTTCGGG TTTACTTTCT AAGGAAAGCC GAGCGGAAAGC TGCTAACCTG GGAATCGGTG 60
 CATAAGGAGA ACTTTCTGCT CGCACCGCT AGGGACAAAGC GGGAGAGGGA CTCCGAGGT 120
 CTGAAGCGCA CGTCCCGAGA GTGGACTCTG GCACTGAAC AGCTGGGACA CATCCGGCAG 180
 TAGAACACAGC GCGTGAAGT GCTGGAGCGG GAGGTGCGAC AGTGTAGCGG CGTCTGGGG 240
 TGGGTGGCGG ANGCCATGAC CGCTCTGCTT TGCTGCCCTC ANGTGGGGCG CCACCCCTG 300
 ACCTGCTGG GTCTTAAACAGC TGAGCTCTG TGCGGACTCT CAAGGAAAC CCCACACNG 360
 GGATTTCTG CCTANANTAA GGTCATCTG GGCCTGGGCC CCCCACTCTG GTTGGCTTG 420
 TCTTTGANGT GAGGGCATG TCCATCTGGG CCACCTGCTG GACCACCTT NGGGAGTGT 480
 CTCCTTCAAAC CCACANNATG CGCCGGCTCTC CGGGAAACC ANTCCCANCC TGNGAAGGT 540
 CAAGNCCTGN ATCCACTNT NCTANAAACCG GCCNCNCNC CGTGTGAACC CNCCCTNTN 600
 TCTCTTCTN TNAAGGTTAA TNNCGCTTGC GCCTTNCAN NGTCCNCNC NTTTTCCNN 660
 GTTNAATATG TTANGCNCAAC NCCNNTCCN CNNCNNCNAN CCCGACCCNN ANNTTNNANN 720
 NCCTGGGGT NCCNNNGAT TGACCCNNCC NCCTNTANT TGCTTNGGG NNCNNNTGCC 780
 CTTCCTCTG NGGGANNGC 799

(2) INFORMATION FOR SEQ ID NO:9:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 801 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

ACGCCCTTGAT CCTCCCAAGG TGGGACTGGT TCTGGGAGGA GCGGGCATG CTGTGGTTTG 160
 TAANGATGAC ACTCCAAAG GTGTTCTGA CACTGGCCA GATGGACATG GGGCTCACCT 120
 CAAGGACAAAG CGCACCAAGGT GCGGGGGCG AAGCCACAT GATCCTACT CTATGAGCAA 180
 AATCCCTGT GGGGCTTCT CCTTGAAGTC CGCCANCAAGG GTCAGTCTT TGACCCCG 240
 CAGGTATGG GTTGTNGNC CAACTGGGG CCNCAAGCA AAANGCNCA GGGCCTCNGN 300
 CACCCATCCC ANGACGCGGC TACACTNCTG GACCTCCNC TCCACCACTT TCATGGCTG 360

TTCTNACCGG CGNATNTGTC CCANCTGTTT CNGTGCNAC TCCANCTTCT NGGACGTGCG 420
 CTACATACGC CGGGANTCNC NCTCCCGCTT TGTCCTATC CACGTNCCAN CAACAAATT 480
 CNCCNTANTG CACCNATTCC CACHTTNNC AGNTTTCNCN NNNGNCGCTTC CTNTAAAAG 540
 GGTGANCCC CGGAAATNC CCCAAAGGGG CGGGGGCNGG TACCCAACTN CCCCCNTATA 600
 GCTGAANTC CCATNACCCN GNCTCNATGG ANCCNTCCN TTTAANNACN TCTCTNAACTT 660
 GGGANANCC CTCGCCNTN CCCCNTTAA TCCCNCTTG CNANGNCCNT CCCCCNTTCC 720
 NCCNNNTNG GCNTNTNANN CNAAAAGGC CCCCCNAACTTCTCTNNCN CCTCANNTCG 780
 CCACCCCTCG AAATCGGCCN C 801

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 789 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

CAGCTTAATG GGCCAGTGTG GCAGCTTCTC CTGTGGCTGC CGGTGCCACA TGCCTGTC 60
 ACAGTGTGGC CGTGGTGACA GCTTCAGGCC CTCCTACCGG GTTCACCTTC TCAGGCCCTGC 120
 AGATCTGCC CTACACACT GCTCTCCCTT ACCACCGGGA AAAGCAGGTG TTCCCTGCCC 180
 AATACCGAGG GGACACTGGA GTGTGCTAGCA GTGAGGACAG CTCGATGACC AGCTTCTGC 240
 CAGGCCCTAA GCCTGGAGCT CCCCTCCCTA ATGGCACACT GGGTGCTGGA GGCAGTGGCC 300
 TGCTCCACC TCCACCCGGC CTCTGGGGG CTCTCTGC TGATGTCCTC GTACCTGTRG 360
 TGGTGGTGA GCCCAGCGGAG GCCAGGGTGG TCTCGGGGG GGGCATCTGC CTGGACCTCG 420
 CCATCTGGA TAGTGTCTC TGCTGTCCCA NGTGGCCCGA TCCCTGTTTA TGGGCTCCAT 480
 TGTCAGCTC AGCCACTCTG TAECTGCCTA TATGGTGTCT GCGCGAGGCC TGGGCTCTGGT 540
 CCCATTACT TTGCTACACA GGTANTATTG GACAAGAACG ANTIGGCCAA ATACTCAGGG 600
 TTAAAAATT CCAGCAACAT TGGGGTGGG AGGCTCTCT CACTGGCTCC AACTCCCCCG 660
 TCCGTGTAAC CCCATGGGGC TGCCGGCTCTG GCGGCCRAAT TCTGTGTCG CCAAANTNAT 720
 GTGGCTCTCT GCTGCCACCT GTTGTGCTG GAAGTCNTA CNGCNCANCNT NGGGGGTNG 789
 GGNGTCTCC

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 772 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

CCCACCCCTAC CCAAAATATTA GACACCAACA CAGAAAAGCT AGCAATGGAT TCCCTTCTAC 60
 TTGTTAAAT AAATAAATTA AATATTTAA TGCCCTGTGTC TCTGTGATGG CAACAGAAGG 120
 ACCAACAGGC CACATCTGTA TAAAGGTAA GAGGGGGGGT GATCAGCAAA AAGACAGTGC 180
 TGTGGGCTGA GGGGACCTGG TTCTGTGTT TGCCCTCTA GGACTCTTC CCTACAAATA 240
 ACTTTCTAT GTTCAATCC CATGGAGGG TGTTCTATCC TAGAAACTCC CATGCAAGAG 300
 CTACATTTAA CGAAGCTGCA GTTAAAGGGG CTTANAGATG GGAACCAGG TGACTGAGTT 360
 TATTCTAGTC CAAAAAACCC TTCTCTAGGT GTGTCTAAC TAGGAGGCTA GCTGTAAACC 420

CTGAGCCTGG	GTAATCCACC	TGCAGAGTCC	CCGCATTCCA	GTGCATGGAA	CCCTTCTGGC	480
CTCCCTAT	AAAGTCAGAC	TGAAAACCCC	TTGGAAAGGCC	TCCAGTCAGG	CAGCCCTANA	540
AACTGGGGAA	AAAAGAAAAAG	GACGCCCCAN	CCCCCAGCTG	TGCACTACG	CACCTCAACA	600
GCACAGGGTG	GCAGCAAATAA	AACCACTTTA	CTTTGGCACCA	AACAAAACCT	NGGGGGGGCA	660
ACCCGGCAC	CCCNANGGG	GTTAACAGGA	ANCNNGGNA	CNTGGAACCC	AATTNAGGCA	720
GGCCNCAC	CCCAATNTT	GCTGGGAAAT	TTTCTCC	CTAAATTTT	TC	772

(2) INFORMATION FOR SEQ ID NO:12:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 751 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

GCCCCAATT	CAGCTGCCAC	ACCAACCAAG	GTCAGTCGAT	TAGTTCGGAT	GTCACTACAAA	60
AGCTGATTGA	AGCAACCACTC	TACTTTTG	TCGTGAGCCT	TTTGTGAGT	GCAGGTTCAC	120
TTGGCTGTG	TGGTGACGTT	GTCACTGCA	CAGAATGGGG	GAAAGGCACT	GTTCCTTGT	180
AAAGTANGG	TGTCCTCAA	ATCCGTATAG	TTGGTGAGC	CACAGCACTT	GAGCTCTTTC	240
ATGGTGTGT	TCCACACTTG	AGTGTGAGCT	TCTGTGGAAAC	CAAAATCTT	CTTGATGGCA	300
GGCACTACCA	GAACAGTCAG	GGAAAGTGTG	AGCCATTGTC	GTGTCACCCA	AGGC3ACAC	360
AGCAGCTGC	ACCTCAGCAA	TGAAGATGAN	GAGGAGATG	RAGAGAAGC	TNCNGAGGGC	420
ACACTTGTG	TCAGTGTGCA	ACCATCANA	GCCNTGAA	ACCAANANCA	AAGACCAACNA	480
CNCCGGCTG	GATGAAAGAA	TNACCCCNCG	TTGACAATAA	TGCACTGGAC	TGGGACAC	540
AGTGGCCCTNA	AAAATCTTC	AAAAGGATGC	CCCCATCATT	GACCCCTCAA	ATGCCCACTG	600
CCAACAGGG	CTGGCCCAACN	CNNNNACGA	TGANCNNTA	GNACAAAGTC	TNCNTGGTGT	660
TNATNAACNT	GAACCCCTGN	TNGTGGCTCC	TGTTCAAGG	CNNGGCTGA	CTTCTNAANN	720
ANAACTCN	GAAGNCACCA	CNGGANANNC	G			751

(2) INFORMATION FOR SEQ ID NO:13:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 729 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

GAGCCAGGGC	TCCCTCTGCC	TGCCRACTCA	GTGGCAACAC	CCGGGAGCTG	TTTTGTCTT	60
TGTGGANCT	CAGCAGTNCC	CTCTTTCAAGA	ACTTCATGCC	AAGANCCCTG	AAAGGAGGCC	120
ACCATGCGAT	GCTTCAGCTT	CATTAGACC	ATGATGATCC	TCTTCATTTT	GTCATCTT	180
CTGCTGTG	CAGCCCTGTT	GGCAGTGGG	ATCTGGGTGT	CAATGATGG	GGCATCCCTT	240
CTGAAGATCT	TGGGGCACT	GTCTCTCAGT	GGCCATCAGT	TTGTCACGT	GGGCTACTTC	300
CTCTATCGCAG	CCGGCTGTGT	GGTCTTAGCT	TAAGGGTTC	TGGGCTGCTA	TGGTCTAAAG	360
ACTGAGACCA	AGTGTGCGCT	CGTGCACCTTC	TTCTTCATCC	TCCTCTCTAT	CTTCATGCT	420
GAGGTGCAA	TGCTGTGGTC	GCCTTGGTGT	ACACCAACAT	GGCTGAGC	TTCCTGACGT	480
TGCTGTGAT	GCCTGCGCATC	AANAAAAGAT	TATGGTTC	CAGGAANACT	TCACTCAAGT	540
GTTGGAACAC	CACCATGAAA	GGGCTCAAGT	GCTGTGGCTT	CNNCCAACTA	TACGGTTTT	600

GAAGANTCAC CTACTTCAA GAAAANAGTG CCTTTCCCC ATTTCGTGTT CAATTGACAA
 ACGTCCCCAA CACAGCCAT TGAAAACCTG CACCAACCC AAANGGTCC CCAACCANA
 ATTNAGGG 660
 720
 729

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 816 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

TGCTCTTCCT	CAAAGTTGTT	CTCTTGGCCA	TAACAACCCAC	CATAGTAAA	GCGGGCGCAG	60
TGTCGCTGA	AGGGTTGTA	GTACAGCGC	GGGATGCTCT	CCTTGAGAG	TCTCTGTGCT	120
GGCAGGCCA	CGCAGTGGCC	TCTGTCATCG	GGGAAATGGG	TGGCTGTGAG	CTCGTCAGG	180
CCACTCTGT	ATTTTCACAA	GGCAGCTCCG	TCCGACCGGT	CGGGGCAGTT	GGGGGTGTCT	240
TCACACTCCA	GGAAACTCTC	NATGCAGCAG	CCATTGCTGC	AGGGAACTTG	GTTGGGCTGA	300
CANGTGGCAG	AGCACACTGG	ATGCGCCCTT	TCCATGNAN	GGGCCCCTGG	GGAAAGTCCC	360
TGANCCCAN	ANCTGCTCTC	CAANGCCCA	ACCTTGACACA	CCCCGACAGG	CTAGAAATGG	420
ATCTTCTTCC	CGAAGGTAG	TITTTCTGTG	TGCCCANAAC	ANCCCNNTAA	ACAAACTCTT	480
GCANANTCTG	TCCGGNGGGG	TCTNANTACCC	ANCGTGGGA	AAGAACCCCA	GGCNGCGAAC	540
CAANCTTGT	TGGATNTGGA	GCNATAACTT	NCTNTCTC	TTGGTGGACA	GCACCANTNA	600
CTGTTNNACT	TTAGNCNTTG	GTCTCTNTGG	GTGNNCTTG	AACCTAATCN	CCNNTCAACT	660
GGGACAGGT	AAANTNGCCT	CCTTNTAATT	CCCNANCNT	CCCCCTGGTT	TGGGGTTTNTT	720
CNCNCTCTA	CCCCAGAAAN	NCCGTGTCC	CCCCCAACTA	GGGGCCNAAA	CCNNTTNTTC	780
ACAACCCCT	CCCCACCCAC	GGGTCNGNT	GGTTNG			816

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 783 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

CCAAGGCCTG	GGCAGGCATA	NACTTGAAGG	TACAACCCCA	GGAAACCCCTG	GTGCTGAAGG	60
ATGTGGAAA	CACAGATGG	CCCTACTCG	GGGTGACAC	GGATGTCAGG	GTAGAGAGGA	120
AAGACCCAA	CCAGGTGGA	CTGTGGGAC	TCAAGGAANG	CACCTACTTG	TTCCAGCTGA	180
CAGTGACTAG	CTCAGACCC	CCAGAGGACA	CGGCCAAACGT	CACAGTCACT	GTGCTGTCCA	240
CCAGCAGAC	AGAACAGTAC	TGCCCTCGCAT	CCAACAANGT	GGTCTCGTGG	CGGGGCTCTT	300
TCCCAAGCTG	GTACTATGAC	CCACGGGAGC	AGATCTGCAC	GAGTTCTGGT	TATGGAGGCT	360
GCTTGGGCA	CAAGAACAC	TACCTTGGCG	AGAACAGTAC	CATTCTANCC	TGTCNGGTC	420
TGCAAGGTGG	GCCTTGTGAA	NGCANCNTCTG	GGGCTCANG	GACTTTCCCC	CAGGGCCCT	480
CCATGGAAG	GGGCCATCCA	NTGTTCTCTG	GCACCTGTCA	GGCCACCCAG	TTCCGCTGCA	540
NCATGCGTC	CTGCACTNAC	ANTTCTCTG	AATTGTCACA	ACACCCCCCA	NTGCCCCCAA	600
CCCTCCCAAC	AAAGCTTCCC	TGTTAAAAAA	TACNCANTT	GGCTTTTNA	AAACNCACCGG	660
CNCCTCCNNT	TTCCCNNTN	AAACAAAGGC	NCTNGCNTT	GAACTOCCCN	AACCCNGGAA	720

TCTNNCNNNGG AAAAANTNCC CCCCTGGTT CCTNNAAANCC CCTCCNCNAA ANCTNCCCCC
 CCC 780
 CCC 783

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 801 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ_ID NO:16:

GGCCCAATTC	CAGCTGCCAC	ACCACCCACG	CTGACTGCAT	TAGTTGGAT	GTCA	TACACAA	60
AGCTGATTGA	AGCAACCCCTC	TACTTTTGG	TCGTGACCT	TTTGCTTGGT	GCAGGTTTCA	120	
TTGGCTGTGT	TGGTGACCTG	GTCATTGCA	CAAGAATGGG	GAAGGGACT	GTTC	TCTTIG	180
AAGTAGGGTG	AGTCTCAA	ATCGTATAG	TTGGTGAAGG	CAACAGCACT	GAGCCTTC	240	
ATGGTGGTGT	TCCACACTG	AGTGAAGTCT	TCTCTGGAAAC	CATAATCTTT	CTTGATGGCA	300	
GGCACTACCA	GCAACGTCAG	GAAGTCTCA	GCCATTGTTG	TGTACACCAA	GGCGAC	360	
GCAGCTGCAA	CCTCAGCAAT	GAAGATGAGG	AGGAAGATGA	AGAAGAACGT	CNCAGGGCA	420	
CACTTGTCT	CGCTCTTAGC	ACCATAGCAG	CCCANGAAC	CAAGACCAA	GACCAACG	480	
CCNGCTGGA	ATGAAAGAAA	NTACCACCTG	TGACAAACTG	CATGGCCACT	GGACGACAGT	540	
TGGCCCGAAN	AICTTCAGAA	AAGGATGCC	CCATCGATG	AAACCCANNA	TGCCCAGTC	600	
CNACAGGGCT	GCNCNCNCN	GAAAGAATGA	GCCATTGAG	AAGGATCNTC	NTGGTCTTAA	660	
TGAACTGAAA	CNTGACATG	TGGCCCTGT	TCAGGGCTCT	TGGCAGTGA	TTCTGNAAA	720	
AAGGAACNGC	NTNAGCCCC	CCAAANGANA	AAACCCCCC	GGGTGTTGCC	CTGAAUTGGC	780	
GGCCAAGGAA	CCCTGCCCCN	G				801	

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 740 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ_ID NO:17:

GTGAGAGCCA	GGCGTCCCTC	TGCCTGGCCA	CTCAGTGGCA	ACACCGGGGA	GCTGTTTGT	60
CCTTTGTGGA	GCCTCAGCAG	TTCCTCTTT	CAGAACTCAC	TGCCAAGAGC	CCTGAACAGG	120
AGCCACCATG	CAGTGTCTCA	GCTTCATTA	GACCATGATG	ATCTCTTC	ATTTGCTCAT	180
CTTTCTGTG	GGTCAGGCC	TGTGCGAGT	GGGCATCTGG	GTGTCATCG	ATGGGCATC	240
CTTTCTGAAG	ATCTTCGGGC	CACTGTCCTC	CAGTGCATG	CAGTTGTC	ACGTOGGCTA	300
CTTCCATC	GCAGCCGGCG	TGGTGTCTT	TGCTCTTGT	TTCTCTGGCT	GCTATGTTGC	360
TAAGCCGGAG	AGCAAGTGTG	CCCTCGTGAC	GTTCTCTTC	ATCTCTCC	TCACTCTTCAT	420
TGCTGAAGTT	CGAGCTGCTG	TGGTGCCTT	GGTGTACACC	AACTATGGT	AACCATCTCT	480
GACGTTGCTG	GTANTGCTG	CCATCAANAA	AGATTATGG	TTCCCAAGGA	AAATTCTACT	540
AAANTNTGGA	CACCCNCCTAG	AAAAGGCTC	CAATTCTGTN	TGGCTTCCCC	AACTATACCG	600
GAATTITGAA	AGANTCNC	TACTTCAAA	AAAAAANANT	TGCCCTTINCC	CNNNTTCTGT	660
TGCAATGAAA	ACNTCCAAN	ACNGCCAATN	AAAACCTGCC	CNNNAAAAA	GGNTCNCAA	720
CAAAAAAANT	NNAAGGTTN					740

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 802 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

CCGCTGGTTG	CGCTGGTCCA	GNGNAGGCCAC	GAAGCACGTC	AGCATAACACA	GCCTCAATCA	60
CAAGGTCTTC	CAAGTCGCCG	AACTTACGCA	GGGAAGAGC	CTTCAGCAAC	ACTGCATATG	120
GGATACACTT	TACTTTAGCA	GCCAGGGTGA	CAÄCTGAGÄG	GTGTCGÄAGC	TTATTTCTCT	180
GAGCCCTGT	TAGTGAGGGA	AGÄTTCCCGG	CITTCAGCTAA	GTAGTCAGGG	TATGTCCTCAT	240
AAGCAACAC	TGTGAGCAGC	GGAAÄGGÄTAG	AGGCAAAGTC	ACTCTCACGCC	AGCCTCTAA	300
CATTGGGCAT	GTCCAGCAGT	TCTCCAAACAA	CGTAGACACC	AGNGGCCCTC	AGCACCCGTAT	360
GGATGAGTGT	GGCCAGGCT	GCCCCCTTGG	CCGACTTGGC	TAGGAGCAGA	AATTGCTCT	420
GGTTCTGCC	TGTCACCTT	ACTTCCCAC	TCTACACTG	ACTGAGTGTG	GGGGACTTGG	480
GCTCAGGATG	TCCAGAGAC	TGTTTCCGG	CCCTCNCTTA	ATGACACCGN	CCANNAACCC	540
GTCGGCTCC	GGCCGANTG	TTCGTCCTNC	CTGGTCAAG	GTCGTCGGC	CNCTACTTGC	600
AANCTTCGTC	NGGGCCATGG	AATTCCACCC	ACGGAAACTC	GTANGATCCA	CINNTTCTAT	660
AACCGGNCG	CACCGCNNTN	GGAACTCAC	TCTTNTINNC	TTTACTTGTAG	GGITAAGGTC	720
ACCCCTTNCC	TTACCTTGTG	CCAAACCNNTN	CNTGTGTG	ANATNTNAA	TCTGNGNCCNA	780
TNCCANCCNC	ATANGAGCC	NG				802

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 731 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

CNAAGCTTCC	AGGTNACGGG	CCGCNAANCC	TGACCCNAGG	TANCANAANG	CAGNCNGCG	60
GAGCCCACCG	TCACCGNNNG	GNGTCTTAT	NGGAGGGGGC	GGAGCCACAT	CNCTGGACNT	120
CNTGACCCCCA	ACTCCCCNC	NCNCNTGCA	GTGATGAGT	CAGAACTGÄA	GGTNACGTGG	180
CAGGAACCAA	GANCAAANNC	TGCTCNHRTC	CAAGTCGGCN	NAGGGGGCGG	GGCTGGCCAC	240
GCNCATCCNT	CNAGTGTG	MAAGCCCN	CCCTGTCTACT	TGTTTGAGA	ACNGCNNNGA	300
CATGCCAGN	GTIANATAAC	NNGGNGAGAG	TNANTTTGCC	TCTCCCTTCC	GGCTGCGCAN	360
CGNGTNTGCT	TAGNGGACAT	AACCTGACTA	CTTAACGTAA	CCCNNGAATC	TNCNCNNCC	420
CCACTAAAGCT	CAGAAACAAA	AACTTCGACA	CCACTCANTT	GTCACCTGNC	TGCTCAAGTA	480
AAGTGTACCC	CATNCCCAAT	GTNTGTNGA	NGCTCTGNCC	TGCTNTTANGT	TGGTCCTG	540
CAAGACCTTAT	CAATTNAAGC	TATGTTTCTG	ACTGCTCTT	GCTCCCTGNA	ACAACNACC	600
CNNCNNTCCA	AGGGGGGCG	GGCCCCAAAT	CCCCCAACC	NTNAATTNAN	TTTANCCCN	660
CCCCCNCGCC	CGGCCCTTTA	CNANCNTC	NNACNGGNA	AAACCNNGC	TTTNCCCAAC	720
NNAAATCCNCC	T					731

(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 754 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

TTTTTTTTT	TTTTTTTTT	TAAAAACCC	CTCCATTNAA	GNNAAACTTC	CGAAATTGTC	60
CAACCCCTC	CAACCCATTN	CCNCTTCCC	GNGGGGTC	CAAACCCAA	TTANNTTGG	120
ANNTAAAT	AAATTTNTT	TGGNGGNNA	ANCCNAATG	NANGAAAGTT	NAACCCANT	180
TNANCNTNA	TNCCTGGAAA	CCNGTNGNTT	CCAAAATNT	TTAACCTTA	ANTCCCTCG	240
AAATNGTTNA	NGGAAAACCC	AANTTCTC	AAAGTTGT	GAAGGNTNAA	TNAAAANCCC	300
NNCCAATTG	TTTNGCCAC	GCCTGAATTA	ATTGGNNTCC	GNTGTTTTC	NTIAAAANAA	360
GNNNANCCC	GGTTANTNAA	TCCCCCNNC	CCCAATTATA	CCGANNTTT	TTNGAATTGG	420
GANCCCNCGG	GAATTAACCG	GGNNNTTCC	TNTGGGGGG	CNGNNNCCC	CCCCNTCGGG	480
GTTTNGGGG	AGGNCNNNAAT	TGTTTAAGGG	TCCGAAAAT	CCCTCCNAGA	AAAAAANCTC	540
CCAGGNTGAG	NNTNGGGTT	NCCCCCCC	CANGGCCCT	CTCGNANAGT	TGGGGTTTGG	600
GGGGCTGGG	ATTTTNTTC	CCCTNTTNC	TCCCCCCC	CNGGGANAG	AGGTTNGNT	660
TTTGTNCNNC	GGCCCNCCNC	AAGANCTT	CCGANNTNA	TTAATACCTNT	GCCTNGGGCA	720
AGTCCNTTGN	AGGGNTAAAN	GGCCCCCTNN	CGGG			754

(2) INFORMATION FOR SEQ ID NO:21:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 755 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

ATCANCCAT	GACCCNAAC	NNGGGACCN	TCANCCGNC	NNNCNACCN	CGGCCNATCA	60
NNNGTAGNNC	ACTNCNTNTT	NATACCNCC	CNCCNACTAC	GGCCNVCNANC	CNACGCNCTA	120
NNCANATNNC	ACTGANNCGC	CGANGTNGA	NGAGAAANCT	NATACCANAG	NCACCCANACN	180
CCAGCTGTC	NANAANGCT	NNNATACNGG	NNNATCCAT	NTGNANCCCT	CNAAGTATTN	240
NNCNCCNAT	GATTTTCTCN	ANCCGATTAC	CCNNTCCCC	TANCCCTCC	CCCCCAACCTA	300
CGAAGGCNCT	GGNCCNAAGG	NNCGCNLNC	CCGCTAGNTC	CCCNNAAGT	CNCCNCNCTA	360
AACTCANCCN	NATTACNCGC	TTCTTGAGTA	TCACTCCCC	AATTCACCC	TACTCAACTC	420
AAAANATCN	GATAACAAAT	AATNCAAGCC	TGNTTATNAC	ACTNTGACTG	GGTCTCTATT	480
TTAGNGGTCC	NTNAANCNTTC	CTAATACTTC	CAGTCNTCT	TNCNCATT	CCNAANGGCT	540
CTTTCNGACA	SCATTTTGTG	GTTCCCNNTT	GGGTTCTAN	NGAATTGCC	TTCTNTGAC	600
GGGCTCTCT	TTTCTTCG	TTANCTGNN	TTCNNCCCG	CAGTTATTAT	TTCCCNNTTT	660
AAATTCTNC	CNTTTTNTC	TGGCNTTNA	AACCCCGCG	CTTGAAGAACG	GGCCCGTGGT	720
AAAGGTTGT	TTTGTGAAA	TTTGTGTTT	GTTC			755

(2) INFORMATION FOR SEQ ID NO:22:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 849 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

TTTTTTTTT	TTTTTGTGTC	GGTAGAGCTT	TACTACAANT	GTGAANACGT	60
ACGCTNNGAN	TAANGCGACC	CGANNTCTAG	GANNCCNCT	AAAATCANAC	120
ATCCCTGNNNA	CGGAAGNGTC	ACCGGNNAT	NNTGCTAGGG	TGNCCTCCTC	180
CATAACTCNG	NGGCCCTGC	CACCACTCNG	GGCGGCCCC	CANNNCNTTN	240
GNNTTAACCN	CACTNNGCNA	NCGGTTTCCN	NCCCNCCNCG	ACCCNGGGC	300
TCTGTCCTTC	CTCTGNGACN	ANAAATGGG	CCNGCGNCCC	TCTTACCCCT	360
CNGCCNTCTA	NCCNCNGC	CCCTCCACNT	NNGGGGACT	GGCNANNGCT	420
NNACCCNNN	GGGTNCTTCG	GTGTCGANT	CNACCGAN	CCANGGATT	480
TGCGTTNTTG	GGCCCTACCC	TTCGCTNCGG	NNCACCCCTC	CAGACNANGA	540
CNCNCNCGN	CCTCNCCTCG	CAACACCCG	NCTCTCNGT	NCGGNNNCCC	600
NCCCTCNNC	NGNGCNANCN	CTCCNCCN	GTCTCANCA	CCCCACCECC	660
NTCANCCACN	GGGNGACNNG	NAACNCGNTC	GCNCCCGGCN	CGGCAGGCC	720
CTNCNTCNGG	CCANTNCNGC	TCAANCCNNA	NAACACCGG	CGNAGCGNCC	780
NCCTCCNCGA	GTCCCTCCCG	CTTCCNACCC	ANGNNTTCCN	CGAGGACACN	840
NNCANGGG					849

(2) INFORMATION FOR SEQ ID NO:23:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 872 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

GGCGAAACTA	TACTTCGCTC	GNACTCGTGC	GCCTCGCTNC	TCTTTTCTC	CGCAACCATG	60
TCTGACNANC	CGGATINGGC	NGATATCNA	AAGNTCGAN	AGTCCAAACT	GANTAAACACA	120
CACACCNAN	AGANAAATTC	NCTGGCTTCC	ANAGTANACN	ATGAAACNNG	AGAACCCANG	180
NGGCGAATCC	TAATNAGGGC	TGGGCCGCCA	ATNTGTCNCC	GTTCATTNTN	CCAGCNTNC	240
CTTCCNACCC	TACNTCTTCN	NAGCTGTCTN	ACCCCTTNGT	CGNACCCCC	NAGGTGCGGA	300
TGGGGTTTNN	NNITGACCGN	CNNCCCTCC	CCCCNTCCAT	NACGANCCNC	CCGCACCCACC	360
NAANNGCNCG	CCNCCCGNNCT	CTTGGCCNC	CTGTGCTNTN	CCCCGTGNGC	CTGGCNCNGN	420
ACCGCATTGA	CCCTCGCCNN	CTNCNNGAAL	NCGNANACGT	CCGGGTTGNN	ANNANCGCTG	480
TGGGNNNGCG	CTCTGCNCCG	GTTCCTTCNN	NCNNCTTCCA	CCATCTTCNT	TACNGGGTCT	540
CCNCGCCTNC	TCNNNCACNC	ECTGGGACG	TNTCTCTTGC	CCCCCTTNA	TCCCCCCCC	600
CCNCTGNNCC	CGNCCCCACCC	NTCATTTNCA	NAACNTCTTC	ACAANNNCCT	GGNTNNCTCC	660
CNANCGNCN	GTCAANCCNAG	GGAAAGGGNG	GGNNCCNNTG	NTTGACGTTG	NGGNGANGTC	720
CGAAANANTC	TCNCNTCNC	TCNTACCCCT	CGGGCGNNCT	CTCNGTTNC	AACTTANCAA	780
NTCTCCCGG	NGNGCNCTC	TCAGGCTCN	CCNCNCNCT	CTCTGCGANTG	TNTCTGCTC	840
TNACCCNNTAC	GANTTTCTGN	CCNCCTCTT	CC			872

(2) INFORMATION FOR SEQ ID NO:24:

- (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 815 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(iii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

GCATGCAAGC TTGAGTATT CATAAGNTCA CCTAAATANC TTGGCCTTAAT CATGGCTNTA	60
NCTGNCTTCC TGTGTCAAAT GTATACNAAT TANATATGAA TCTNATNTGA CAAGANNGTA	120
TCTNTCATTA GTAACAANTG TNNTGTCAT CCTGTGNCAN CAANNTCCCA TNNAATTNCGN	180
CGCATTCTCN GCNCANTAT TAATNGGGAA NTCCNNNTNN NCACCCNNTAT CTATCCTNNCC	240
GNCNCTTGAC TGNNAGAGAT GGATANTNTC TNNNTGACC NACATGTTCA TCTTGGATTN	300
AANANCCCCC CGCNGNCAC CGGTTGNNNG CNAGCCNNTC CCAAGACCTC CTGTGGAGGT	360
AACCTCGCTC AGANNCATCA AACNTGGAA CGCCGNCNNC ANGTTNAACT NGNNNCANAN	420
GATCCGTCTC AGGNTTNACT ATCCCTTCAG AGGCCCTCT TTNGTGCCTT ANAGNGNAGC	480
GTGTCNNANC CNCTCACAT GANAGCCGC AGNCCANCCG CAATTNNGCA CAATGTCGNC	540
GAACCCCCCTA CGGGGNTTGA TNCAANCC CAGGATTTC CNNCANGAA ATCCCNANC	600
CCCNCCCTAC CCNNCTTTG GAACNTGAC AANTCCCGGA GTNCCAGTCC GGCCNGNCTC	660
CCCCACCGGT NNCCNTGGGG GGGTGAANCT CNGNNTCANC CNGNCAGGN NTCGNAAGGA	720
ACCGGNCCTN GNNGCAANNG ANCNCNTTCA AGNGCCNCNT CGTATAACCC CCCCTCNCCA	780
NCCNACNGNT AGNTCCCCCC CGGGGTNCGG AANGG	815

(2) INFORMATION FOR SEQ ID NO:25:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 775 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

CCGAGATGTC TCGCTCCGTG GCCTTAGCTG TGCTCGGCT ACTCTCTCTT TCTGGCTTGG	60
AGGCTATCCA CGGTACTCCA AAGATTCAAGG TTTACTCAAG TCATCCAGCA GAGAATGGAA	120
AGTGCATTCCTT CCGTGTCTG TATGTCTCTG GGTTCTCATC ATCCGACATT GAANTTGA	180
TACTGAAGAA TGGAGAGAGA ATTGAAAAGG TGGAGCATTC AGACTTTGCT TTCAGCAAGG	240
ACTGGCTTTA CTATCTCTG TACTACACTG ATTTCACCCC CACTGAAAAA GATGAGTATG	300
CTTGGCGCTG GAACCATGTC ATTTGTAC AGCCGAAAGAT AGTTAAGTGG GATCCGAGACA	360
TGTAAGCAGN CNNCATGGAA GTTGAAGAC GCGGCATTTG GATTGGATGA ATTCCAATT	420
CTGCTTGTCTT GCNTTTTAAT ANTGTATGC NTATACACCC TACCCCTTAT GNCCCCAAAT	480
TGTTAGGGTT ACATNANTGT TCNCNTNGGA CATGATCTTC CTTATAATT CCNCNTTCC	540
AATTGGCCGT CNCCNCNTT NGAATTTTC CNNAACCCAG GTTGGCTCCC CCAGGTCNCC	600
TCTTACCGAA GGGCCCTGGGC CNCTTCTCA GGTGTTGGGA ACCNAAATT TCNCTTNTGC	660
CCNCCNCNA CNNTCTTGG NCNCANTATT GGAACCCCTTC CNATCCCTT TGGCTCNNA	720
NCCTTNNCTA ANAACCTTN AAACGNTGC NAANNNTTT ACCTCCCCC TTACC	775

(2) INFORMATION FOR SEQ ID NO:26:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 820 base pairs
- (B) TYPE: nucleic acid

(C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26

ANATTANTAC AGTGTAAATCT TTTCCAGAG GTGTGTANAG GGAACGGGGC CTAGAGGCAT	60
CCCANAGATA NCTTATANCA ACAGTGCTT GACCAAGAGC TGCTGGGCAC ATTTCCTGCA	120
GAAAAGGTGG CGGTCCCCAT CACTCTCTC CTCCCATAAGC CATCCACAGG TGAGTAG	180
CCATCANGC TTCAGTGGGA GGGAGTCANG GAAACACANAC CACACAGGC ANACAGACCA	240
NTGATGCCA TGGGGGGGG CGAGCTCTT CCTGTACCGG GGGTGGCANA NGANAGCCTA	300
NCTGAGGGGT CACACTATA ACNTTAAAGC CCNAGATNAN CACCTGCTTC AAGTGCACCC	360
TTCCACTCTG ACNACAGNG ACCNNNAACT GCNGCTGGG GACAGCNCTG GGANCAGCTA	420
ACNNAGCACT CACCTGGCCC CCCATGGCC NCNCCTCTC TGGTCTGNC AAGGGAAACT	480
CCCTGTGGGA ATTNCGGGGA NACCAAGGGG NCNCCTCTC CCANCTGTA AGGAAAAAANN	540
GATGAATTTC TNCCCTCTCCG GCNNNITCCC TCTTCCTTCA CACGCCCTCT NNNTACTCTC	600
TCCCTCTNTT NTCCCTGNNC ACTTITNACC CCCCCNNTTC CCTTNATGTA TCGGANCTN	660
GANATTCAC TNCCCTCTC CNTCNATCNG NAANACNAAA NACTNTCTNA CCCNGGGGAT	720
GGGNNCCTCG TNCCATCTCTT CTTTTCTCT ACCNCNNNT CTTTGCTTC CCTTNGATCA	780
TCCACCCNTC GNTGGCCNTN CCCCCCCTNN TCCCTTNCC	820

(2) INFORMATION FOR SEQ ID NO:27:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 818 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27

TCTGGGTGAT GGCTCTTCTC TCCTCAGGGA CCTCTGACTG CTCTGGCCA AAGAATCTT	60
TGTTTCTCT CCGAGCCCCA GGCAGGGGT ATTACGGCTC CCTCCAACTTG ATTCTGATGA	120
CTGGGGATGC TGTGAGGCAC CCAAGGGCA ATATAGGCTC CAGGGTCCAG GGAGGGGCGC	180
CTGGTGGAGCA TCACCCCTGC CAGCCCCTCG CATGAGCTCT GGCTGGGTG	240
TCCGGCTTCA GGGTTCTGCT CTTTCCANCA NGCCANCAAG TGCGCTGGG CCACACTGGC	300
TTCTTCTCTC CCCNTCCCTG GCTCTGANTC TCTGTCCTTC TGTCCTGTC ANGNCNCTG	360
GATCTCAGTT TTCCCTCTNC ANNGAACCTC TTATCTGANN TCTTCANTTA ACTNTGANT	420
TATNACNAN TGGNCTGTC TGTCNNACTTC TATGGGCTA GACCGGCTAA TCCCTCTCC	480
NCTCCCTCTC ANTTCCNNNA ACCNGCTTC CNTCNCTCC CNTNACCCG CCNGGGAANC	540
CTCCCTTGCC CTNACCAAGG GCCNNNACCG CCNTNNTCTN GGGGGCNNG GTNNCTNC	600
CTGNTNNCC CNCTCNCTN TNCCCTGTC CNNCNNCCG NGCANNNTC NCNGTCCCN	660
TNNCTCTCN NGNTTCGNAA NGNTCNCTN TNNNNNNCN NGNTNTNCN TCCCTCTCNC	720
CNNNTGANG TNNTTNNNNC NCNGNNCCCG NNNNCNNNNN NGNNNTNNN TCTNCNCNGC	780
CCCNCCCCC NGNATTAAGG CCTCCNNCTC CCGCCNC	818

(2) INFORMATION FOR SEQ ID NO:28:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 731 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

AGGAAGGGCG GAGGGATATT	GTANGGGATT GAGGGATAGG AGNATAANGG	GGGAGGTGTG	60
TCCCAACATC ANGGTGNNGT	TCTCTTTGAA ANGAGGGTGTG	NGTTTTTANN CCNGGTGGGT	120
GATTTAACCC CATTGTATGG	AGNNAAAAGGN TTTNAGGGAT	TTTCGGCTC TTATCAGTAT	180
NTANANATCTT CGTAGTGGCAT	TTTNGGGGGN CNGCCANGTT	TCCCAAGGCCTG CTANAACTCGT	240
ATTNCCTCCC GGACTCTG	AATNTATNNT TCNNCNGGAA	ACAGNATCCN TACCCGACTG	300
ACTAAAGNTT NAAGTGGGAN	TNCAATGAA AACTTNNAAC	TCNNCNGNAT GTCNCCNGN	360
TNNNTTNCCTT CGCCCTTNTG	ACTCTGCGN	ACCCAAATAC CCNNGNGNAT	420
CGTTTCNCAT NAAGGCCATT	TNGCCTCATC	GGGTTTTCGCA TCAAAGCNC	480
NGGTTNCCT ACCTCTNNNTG	CNCCTNNNTG	CCCTCNCCCA TTINGCCGTC	540
GNAATGGGTA GGGNCTTNTG	TTTTNACCN	CGGCCTNNGG NAANCCCTC	600
TCTCNACCC CCCCTTTTT	CAATCCANC	GGCNAATGG GTCTCCCCNN CGANGGGGG	660
NNNCCANNC C			720
			731

(2) INFORMATION FOR SEQ ID NO:29:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 822 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

ACTAGTCCAG TGTGGTGGAA	TTCCATGTGT TTGGGNCNC TTCTATGANT	ANTNTAGAT	60
CGCTCACACC	TCACANCTC CCNACNANG	CTATAANGAA NANNAATAGA	120
ATNTNTACNC	TCATANNCCT	CNNNACCCAC TCCCCTCTAA	180
TNNCTANTCT	NTGCGCCCTIN	CNANACCCACN	240
TCNCCATNTN	GCCTANANTA	GTNCTACACC	300
TCCATNANTT	ANNNTAACTA	CAACTGACNT NGACTTCTNC	360
TACTCTGACT	CCACCGCCCT	ATNACCTT AATTGAAATC	420
NTCAACACC	TATCTACTG	ANNNATAGC ANCCTCCCG	480
CCAATACCC	TTCNCAACCC	ANNNATAGC ANCCTCCCG	540
CCACTGGAT	NCCACTCTGAC	ANNNATAGC ANCCTCCCG	600
AATNTCTCTN	NAATTCTACTN	ANNNATAGC ANCCTCCCG	660
TANATCCCTT	CTTICGAAAA	ANNNATAGC ANCCTCCCG	720
CCNAATGAA	CNACCCCTT	ANNNATAGC ANCCTCCCG	780
CCNAATGAA	CNACCCCTT	ANNNATAGC ANCCTCCCG	822

(2) INFORMATION FOR SEQ ID NO:30:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 767 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

CGGCCGCTG CTCTGGCACA TGCCCTCTGA ATGGCATCAA AAGTGTGGA CTGCCCATG 60
 CTAGAGAAGA CCTCTCTCC TACTGTCAATT ATGGAGCCCT GCAGACTGAG GGCTCCCTT 120
 GTCTGAGGA TTTGATGTCT GAAGTCGAGG AGTGTGGCTT GGAGCTCTC ATCTACATNA 180
 GCTGAAAGCC CTGGAGGGCC TCTCTCGCA GCCTCCCCCT TCTCCTCCACG CTCGCCANG 240
 ACACCAAGGG CGCCAGGCAG CCCATTAATCGCAGNANGAC ATGGTGTTC TCCACGGGA 300
 CCCATGGGC CTGNAAGGCC AGGGCTCTCTT TTGACACCAT CTCTCCCTG C1GCCGTGCA 360
 GGCCCTGGGA TCCAATCTT CTANAACGGN CGCCACCCNG CGGGAGGCTC CAGCITTTGT 420
 TCCCNNTAAT GAAGGTTAAT TGNCCTCTG JCGTAAATCAT NGGTCAANAC TNITTCCTGT 480
 GTGAATTGT TTNITCCCTC NCNATCCNC NCNACATACN AACCCGGPAN CATAAAACTGT 540
 TAAAGCTG GGGTNGCCTN NNGAATNAAC TNAACTCAT TAATTGGCCTT GGCTCATGGC 600
 CCGCTTCCN TTCTNGAAAAA CTGCTCTCCC CTGCTNTNT GAATCGGCCA CCCCCCNNGG 660
 AAAAGCGTT TGCTNTTITG GGGGNCTCTT CCNCTTCCCC CCTCNCATAAN CCTCTNCCT 720
 CGGTGTTNC MGGTNGCCGG GAANGGGNAT NNNTCCCN NAAGGGGGNG AGNNNGNTAT 780
 CCCCCAA 787

(2) INFORMATION FOR SEQ ID NO:31:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 799 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

TTTTTTTTTT TTTTTTTGGC GATGCTACTG TTAATTGCA GGAGGTGGGG GTGTGTGAC 60
 CATGTACAG GCGTATTAGA AGCAAGAAGC AGGAAGGGAG GGCAAGACGCC CCTGCTGAGC 120
 AACAAAGAC TCTCTGAGCC TTCTCTGCT GTCTCTGCG GCAGGACAT GGGGAGGCTT 180
 CCCGAGGGT GGGGGACCC AGTCCAGGG TGGGAGCACT ACANGGGGTG GGAGTGGTG 240
 GTGGCTGGTN CNAATGGCTC GNACANACATE CCTAUGATTC TTGACACCTG GATTTCACCA 300
 GGGGACCTTC TGTTCTCCA NGGNAACTTC NTINNATCTCN AAAAGAACACA ACTGTTCTT 360
 CNGCANTTGT GGCTGTTGAT GGAAAGCACA GTGTCCTNAT TTNGGCTGG ACTTGGTACA 420
 TATGGTTCCG GCCCACCTCT CCNTCTNAAN AAGTAATTCA CCCCCCCCN CCNTCTNTG 480
 CCTGGGCTCT TAANTTACCA CACCGAAACT CAINTTANTTA TTCACTCTTNG GNTGGGCTTG 540
 NTNATCCCN CCTGAANGGCG CCAAGGTGAAGGCCACGCC GTNCCCNCTC CCCATAGNAN 600
 NTTTTNNCTC CANTAATGC CCCCCCNGGC AACNATCCAA TCCCCCCCCCN TGGGGGCC 660
 AGCCCCANGGC CCCCGNCTCG GGNNNCCNCG NCNGNANTTC CCAGGNTCTC CCANTCNGNC 720
 CCNNNGCNCC CCCGACGCA GAACANAAGG NTNGAGCCNC CGCANNNNNN NGGTNNCNAC 780
 CTCGGCCCCC CCNNCGNNG 799

(2) INFORMATION FOR SEQ ID NO:32:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 789 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

(2) INFORMATION FOR SEQ ID NO:33:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 793 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ_ID: NO: 33

(xi) SEQUENCE	60
GACAGAACAT GTTGGATGGT GGAGCCCTT TCTATACGAC TTACAGGACA GCAGATGGGG	120
AATTATCGC TGTTGGAGCA ATANAACCCC AGTCTACGA GCTGCTGATC AAAGGACTTG	180
GACTAAGTC TGATGAACTT CCCCATAAGA TGAGCTATGG TGATGGGCCA GAATGAANAA	240
AGAAAGTTGC AGATGTTATT GAAAAGAAGA GCAAGGGACA GTGGTGTCAA ATCTTTGACG	300
GCACATGTC TGCTGTGACT CGCGTCTGAG CTTTGGAGGA GTGTTGTCAT CATGATCACA	360
ACAAANGAACG GGGCTCGTT ATCACCCANTG AGGAGCAAGGA GTGAGGCCCG CCCTCTGAC	420
CTCTCTGTTT AAACACCCCA GCCATCCCTT CTTCACAAAGG ATGGCTACCA CCTTCTAGAGC	480
GNGNCGACC CGGGTGGAGC TCCAGCTTTT GTTCCCTTTA GTGAGGGTTA ATTCGGCCGT	540
TGGCGTAATC ATGGCTCATAN CTGTTTCTGCT TGTTGAATTC ATGGCTTCAT ACAAATTCCAC	600
ACACATACAG ANCCGGAAAGC ATNAAAATTTC AAAGCTCTGGN GTTNGCCCTAA TGANTGAAC	660
NACTCATCATT AATTGGCTT CGCTCTACTG CCCGCCTTCC ATGGCCGGAA ACCTGCTTCCTT	720
GCCAGCTGCC NTAAATGAAAT CNGGCCACCC CCCGGGGAAA AGGCCTGTTT CTNTTGGGG	780
CGNNCTTCCTC GCTTCTCGC TTCCCTGAANT CTTCCCCCCC GCTTCTTCGG CTGCGGCNA	793
ACGGTATCNA CCT	

(2) INFORMATION FOR SEQ ID NO:34:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 756 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(iii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

GCGCGGACCG	GCATGTACGA	GCAACTCAAG	GCGGAGTGGAA	ACCGTAAAG	CCCCAATCTT		60
ANCAAGTGCG	GGGAANAGCT	GGGTCGACTC	AAGCTAGTTTC	TTCCTGGAGCT	CAACTTCTTG		120
CCAACACAG	GGACCAACAGT	GACCAACAG	CAGCTTAATTC	TGGCCCGTGA	CATACTGGAG		180
ATCGGGGCC	AAATGGGACAT	CCTACCGAAN	GACATCCCCCT	CTTCGAGCGC	CTACATGGCC		240
CAGCTCAAT	GCTACTACTT	TGATTACCAA	GAGCACGCTCC	CCGAGTCAGC	CTATATGCA		300
CAGCTTGGG	GCCTCAACCT	CTCTTCTCTG	CTGTCCCAGA	ACCGGGTGGC	TGANTNCAC		360
ACGGANTTGG	ANCGCTGCG	TCCCCAANGA	CATACANACC	AATGTCATCA	TCNACCAACCA		420
GTGTCCTGGA	CGAACATCTGA	TGGANGGCAG	CTACCCNAAA	GTNTTCTCTGG	CCNAGGGTAA		480
CATCCCCCGC	CGAGAGCTAC	ACCTTCTCTCA	TTGACATCTC	GCTCGACACT	ATCAGGGATG		540
AAAATCGGG	CGTTGCTCTCA	AAAGGGCTNC	AAANAATCC	TTTCNCCTGA	AGGCCCCCGG		600
ATINCNCTAGT	NCTAGAATCTC	GCCCCCATC	GGCGTGGGAN	CTCCARACCTT	TGTTTNCCT		660
TTACTGAGGG	TTINATTGCGG	CCCTTGGCGT	TATCATGGTC	ACNCCNGTTN	CCTGTGTTGA		720
AAATTNTAAC	CCCCCACAT	TCCACCGCNA	CATTTNG				756

(2) INFORMATION FOR SEQ ID NO:35:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 834 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

GGGGATCTCT	ANATCNACCT	GNATGCATGG	TTGTCGGTGT	GGTCGCTGTC	GATGAANATG		60
AAACAGGATCT	TGCCCCTTGAA	GCTCTCGCT	GCTGTNTTCA	AGTTGCTTCAG	TCTGCGGTCA		120
TAGTCGACA	CNCNTCTGGG	CAAAAAACAN	CAGGATNTGA	GTCTTGATTCT	CACCTCCAA		180
AATCTTCNGG	GCTGTCTGCT	CGGTGAACCT	GATGACNAGA	GGCAGCTGGT	TGTGTTNTGAT		240
AAANTCCANC	ANGTTCTCTC	TGGTGAACCTC	CCCTTCAAAAG	TGTGTCGGC	CTTCATCATCAA		300
CTTCTTNNAN	ANGANNNANCC	CANCTTTGTC	GAGCTGGNAT	TTGGANAAACA	CGTCACTGTT		360
GGAAAAGTAT	CCCAAATGTT	ATGTCATCTCA	TGGCCCTCTCG	TGCCCTGCAA	AAACTTGTCTT		420
GGCNCNAATC	CGACTTCCCN	TCCCTTGAAAG	AAAGCNATACA	CACCCCTCTC	CCCTGGACTCC		480
NNCAANAGG	CTNCCTGCTC	CCCTNTCCNN	CAGGGTTGGT	GGCANNCCGG	GGCCNTGCGC		540
TTCTTCAGGC	AGTTCACNAT	NTTCATCGGC	CCCTCTGCCA	GCTGTTTNTAT	TCCCTGGGGG		600
GGAAANCCGTC	TCTCCCTTC	TGAANNAACTT	TTGACCGTNG	GAATAGCCGC	GCNTCCNCNT		660
ACNTNCCTGG	CCGGGTCTCAA	ANTCCTCCN	TTGACCGTNG	GAATAGCCGC	GCNTCCNCNT		720
NCCNNACTTT	TTCCCTTCCCC	CNCCCCNCCG	NGTTGGGNTT	TTTCATNGGG	CCCCAACTCT		780
GCTNTTGGCC	ANTCCCCCTGG	GGGNTNTAN	CNCCCCNTNT	GGTCCCNNTNG	GGCC		834

(2) INFORMATION FOR SEQ ID NO:36:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 814 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

CGGNCGCTT	CCNGCCGCGC	CCGGTTTCCA	TGACNAAGGC	TCCCTTCANG	TTAAATACNN	60
CCTAGNAAC	ATTAAATGGT	TGCTCTACTA	ATACATCATA	CNAACCAGTA	AGCCCTGCCA	120
NAACGCCAAC	TCAGGCCATT	CCTACCAAAG	GAAGAAAGGC	TGGTCTCTCC	ACCCCTGTAA	180
GGAAGGCC	GCCTTGTAAAC	ACACCAACAT	NCGGCTGAAT	CTNAAGTCCTT	GTGTTTTACT	240
AATGGAAAAA	AAAATAAAC	AAANAGGTTT	GTTCATGG	CTGCCACCG	CAGCCCTGGCA	300
CTAAACACN	CCAGCGCTCA	CTTCTGCTTG	GANAATATT	CTTGTCTCTT	TTGGACATCA	360
GGCTTGATCG	TATCCTGCG	ACNTTTCAC	CCAGCTGGC	NCCCCCCCC	CATNTTGTG	420
ANTGACTGG	AAGGCTGTAA	NCTTAGTC	CAAAGTCTC	NGCCCACAAG	ACGGGCCACC	480
AGGGGAGTC	NTTTCAGTG	GATCTGCCAA	ANANTACCCN	TATCATCENN	GAATAAAAAG	540
GCCCTGTAAC	GANATGCTTC	CANCANCTT	TAAGACCCAT	AATCCTNGAA	CCATGGTGGC	600
CTTCGGTCT	GTATCCNAAG	GAATTTCTT	GGGTCCCAN	CCCTCCCTTG	TTNCTTACGT	660
TGTTTGTGAC	CCNTGCTNGN	ATNACCCAA	TGANATCCCC	NGAAGCACCC	TNCCCCCTGGC	720
ATTGAGTT	CNTAAATCTC	CTGCGTACT	NCTGAAAGCA	CNATTCCTN	GGCNCCNAAN	780
GGNGAUCTCA	AGRAAGGCTTN	NGAAAACCA	CNCN			814

(2) INFORMATION FOR SEQ ID NO:37:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 760 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

GCATGCTGCT	CTTCCTCAA	GTGTTCTTG	TTGCCATAAC	AACCAACATA	GGTAAAGCGG	60
GCGCAGTGT	CGCTGAAGGG	GTGTTAGTAC	CAGGGCGGA	TGCTCTCTT	GCAGAGTCCT	120
GTGTCCTGCA	GGTCCACCGA	ATGCCCTT	TCACTGGGA	ATGGAATGCG	CTGGAGCTCG	180
TCNAANCCAC	TCTGTATTT	TTCACANGCA	GCCTCTCCG	AAGCNTCCGG	GCAGTTGGGG	240
GTGTCGTGAC	ACTCCACTAA	ACTGTGATN	CANACGCCA	TTGCTGCGC	GGAACTGGGT	300
GGGGTGACAG	GTGCCAGAAC	ACACTGATN	GGCTTTCGA	TGGAAGGGCC	TGGGGGAAT	360
CNCCNTANCC	CAACATGACCT	CTAACAGGCC	ACCTTGCACA	CCCCACAGG	CTAGAAATGC	420
ACTCTCTTC	CCAAAGGTAG	TTGTTCTTG	TGCCCAAGCA	NCCTCCANCA	AACCAAAANC	480
TTGCAAAATC	TGCTCCCTGG	GGGTCACTNNN	TACCANGTT	GGGAAANAA	ACCCCGCN	540
GANCCNCCCT	GTGGAATGC	NAAGGNAATA	ATCCTCTGT	CTGCTTGGG	TGGAANAGCA	600
CAATTGAACT	GTAAACNTTG	GGCCGNNTTC	CNTCTGGGT	GTCTGAACCT	AATCACCCTGC	660
ACTGGAAAAA	GGTGTGTC	TTCTCTGAT	TCCCAANNT	CCCTCTGNTT	TGGGTNTTTT	720
CTCCCTCNCC	CTAAAATCG	TNTTCCCCCC	CNTCTANGCG			760

(2) INFORMATION FOR SEQ ID NO:38:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 724 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

TTTTTTTTT	TTTTTTTTT	TTTTTTTTT	TTTTTTAAA	CCCCCTCCAT	TGAATGAAAA	60
TTTCCNAAT	TGTCCAAACCC	CCTCNCCAA	ATNNCCATT	CCGGGGGGG	GTTCCTAAC	120

CAAATTAATT TTGGANTTTA	ATTTAAATNT	TNATTNNGGG AANAANCCAA	ATGTNAAGAA	180
ATTTAACCC ATTATNAACT	TAATATNCCTN	GAACACCNTG	GNTTCAAAA ATTTTAACC	240
CTTAATTC CTCGAAATG	NTAANGGAAA	ACCAAATCN	CCTAAGGCTN	300
NGATTTAAC	CCCCNTNANT	TNTTNTNACC	CNNGNCTNAA NTATTNTNGNT	360
TCCTNTTAAN	CNTINGGTAC	TCCCNGTAAAT	GAANNNNCCT AANCCCAATT AACCGAATT	420
TTTTGAATT	GGAAATTCM	NGGGAATPTNA	CCGGGGTTTT	480
CCCNCTTCCG	GGGTTTGGGN	NTAGGGTGA	TCCCNNTTGG	540
AAAAAAATCC	CAAGNNTTAA	TTNGAATNTC	GGGCCATNCC	600
TTTNTGGGG	CCNGGGANTT	CNTTCCCCCN	NCCCAAAAAA	660
NGNNNTTGTG	TTTGGGGCC	CTTNANGGAC	CCCGGGNNGT AAANGTTAT	720
GGCG		CTTCGGATN	GAAATTAAT CCCCGGGNC	724

(2) INFORMATION FOR SEQ ID NO:39:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 751 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

TTTTTTTTT TTTTCTTG	CTCACATTA	ATTTTATTT	TGATTTTTT TAATGCTGCA	60
CAACACATA	TTTATTCTAT	TTGTTTCTT	TATTCATTT	120
TTTTTATTT	TTTACTGAA	GTGAGAGGA	ATTTTGTG	180
GGCGCCCTTA	AGCTTCTTA	ATTGGAAACAA	CTCTAAGCAAG	240
CGCAAAATCA	CTCGGGGGAA	NGGAAAGGTT	GCTTGTAA	300
TTAACTGCTT	GTACAATTAC	NTTCACTT	TAATTAATTG	360
CTTGGGGTT	CCCTCCCAN	ACCAACCCCN	TGCTNAANGC	420
TCCGGGCNT	CNTTGAACAA	CAACGGNGAA	GTGCCNGCC	480
TGAAGGGTTA	CCATNTTAA	CCNGCNGAA	TCAAATNATG	540
CCCTCAANCN	AATTNTCTNG	CCCCGTCNC	GTCTGAATCC	600
CACCCCCNGA	ANNCNNNTNC	NAACNAAAATT	TGCTNNTGCT	660
CNNAGACTNT	CCTCNCNC	CNAATTTT	TCCTNNTNC	720
NNNNCNCTC	CNTCTGACCN	NAATNCNCA	GAACNGGNCC	751

(2) INFORMATION FOR SEQ ID NO:40:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 753 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

GTGGTATTTT	CTGTAAAGATC	AGGTGTCTCT	CCCTCGTAGG	60
AGATGAAAC	CCCCCGAGA	CAGCAGCACT	GCACATGCCA	120
CGCCCTATGC	ACAGCTGGC	CCTTGAGACA	GCAGGGCTTC	180
TGGTCTGGAA	GCGGGGGCTG	TACCTGCGTA	GTCAGGGCCC	240
TCTCAAAGTT	CCAGGCAACN	TCGTTGCGAC	ACACCGGAGA	300

CGGTCATAAN CGGGTGGCG TCGTCGCTGG GAGCTGGCG	GGCCTCCCG AGGAAGGGNA	360
ATAAAAGGTG CGCCCCCGCA CCGTTCANCT CGCACTTCCTC	NAANACCATG ANGTTGGGCT	420
CNAACCCACC ACCANNCCGG ACTTCCTTG A NGGAATTCCC	AAATCTCTTC GNCTTGGGC	480
TTCITNCIGAT GCCCTACTNGT GTTGCCTCNGA ATGCCAANCA	NCCCCAANCC CCGGGGTCCT	540
AAANACCCCN CCTCCTCNNT TCATCTGGGT TNTINTCCCC	GGACCNNGGT TCTCTCAAG	600
GGANCCCATA TCTCNACCAN TACTCACCN NCCCCCCNT	GNNACCCANC CTTCCTANNGN	660
TTCNNCCCG NCCTCTGGCC CNTCAAANAN GCTTNCACNA	CCTGGGTCTG CCTTCCCCCC	720
TNCCCTATCT GNACCCCN TNTGTCTCAN TNT		753

(2) INFORMATION FOR SEQ ID NO:41:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 341 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

ACTATATCCA TCACAACAGA CATGCTTCAT CCCATAGACT TCTTGACATA	GCCTCAATG	60
AGTGAACCCA TCCCTGATTAT ATATACATAT ATGTTCTAG TATTTGGGA	GCCTTTCAC	120
TCTTTAAAC CTTGTTCAATT ATGAAACACTG AAAATAGGA	TGGTGAGA GTTTAAAAAGT	180
TATAGCTGT TTACGTAGTA AGTTTTGAA GTCTACATTC AATCCAGACAGA	CTTAGTTGAG	240
TGTTAACTG TGATTTTAA AAAATATCAT TTGAGAATAT TCTTCAGAG	GTATTTTCAT	300
TTTTACTTT TGATTAATTG TGTTTTATAT ATTAGGGTAG T		341

(2) INFORMATION FOR SEQ ID NO:42:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 101 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

ACTTACTGAA TTTAGTTCTG TGCTCTTCCT TATTTAGTGT	TGTATCATAA ATACTTTGAT	60
GTTCACAAACA TTCTAAATAA ATAATTTCAT A		101

(2) INFORMATION FOR SEQ ID NO:43:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 305 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single

- (D) TOPOLOGY: linear
- (iii) MOLECULE TYPE: cDNA
- (vi) ORIGINAL SOURCE:
- (A) ORGANISM: *Homo sapiens*
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:

ACATCTTGT TACAGTCTAA GATGTTCT TAAATCACCA TTCCCTTCGG GTCCCTCACCC	60
TCCAGGGTGG TCTCACACTG TAATTAGAGC TATTGAGGG TCTTACAGC AAATAAGAT	120
TCAGATGCC TGTCAAGTCT AGAGTTCTAG AGTTAGTTT CAGAAAAGCTCT AAGAAACCCA	180
CCTCTTGAGA GGTCACTAA GAGGACTTAA TATTCTCAT ATCAAAATG ACCACAGGAT	240
TGGATACAGA ACGGAGAGTTA TCCCTGGATAA CTCAGAGCTG AGTACACTGCC CGGGGGCCGC	300
TCGAA	305

(2) INFORMATION FOR SEQ ID NO:44:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 852 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (vi) ORIGINAL SOURCE:
- (A) ORGANISM: *Homo sapiens*
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:

ACATAAATAT CAGAGAAAAG TAGCTTTGA AATATTTACG TCCAGGAGTT CTTTGTCT	60
GATTATTGG TGTTGTTTT GGTTGTGTC CAAAGTATG GCAGCTTCAG TTTCATTCTT	120
CTCTCCATTC TCAGGCATTC TTCCCCAATT TATATACCAAG TCTTCGTCAC TCCACACGCT	180
CCAGAATTTC TCTTTGTAG TAATATCTCA TAGCTCGCTC AGCTTTCA TAGGTCTATGC	240
TGCTGTGTT CTTCTTTTA CCCCATAGCT GAGCCACTGC CTCTGATTTC AAGAACCTGA	300
AGACGCCCTC AGATCTCTC TCCCATTTA TTAATCTGG GTTCTGTCTT GGGTTCAAGA	360
GGATGTGCCG GATGAATTCC CATAAGTGC TCCCTCTCGG GTTGTGCTT TTGGTGTGGC	420
ACTTGGCAGG GGGGTCTTG TCTCTTTCA TATCAGTGA TCTGCAACA GGAAGGTGAC	480
TGGTGGTTGT CATGGAGATC TGAGCCGGC AGAAAGTTT GCTGTCACAA AAATCTACTG	540
TGCTACCATCA GTTGGTGTCA TATAATAGT TCTNGTCTT CCAGGTGTC ATGATGGAAG	600
GCTCAGTTG TTCAGTCTG ACAATGACAT TGTGTGGA TGGAACAGG TCACTACTGC	660
ACTGGCCGT CCACCTCTC TCTGTCAAGT TGCTGTAGAG GAGNTGCCGC GCGCTCCCTG	720
CCGCCCGGT GAACCTCTC AAACATCATGC TGCAAAGGTG CTGCCCGTGG ATGTGAACT	780
CNTGAAAGG GATAACAATTG GCATCCAGT GGTGTTGTGTC CAGGAGGTGA TGGAGCCACT	840
CCCACACCTG GT	852

(2) INFORMATION FOR SEQ ID NO:45:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 234 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:45:

ACAAACAGACC	CTTGCTCGT	AACGACCTCA	TGCTCATCAA	GTTGGACGAA	TCCGTGTCCG	60
AGTCTGACAC	CATCCCGACG	ATCAGCATTC	CTTGCAGCTG	CCCTACCGCG	GGAAACTCTT	120
GCCTCGTTTC	TGGCTGGGGT	CTGCTGGCGA	ACGGCAGAAT	GCCTACCGTG	CTGCAGTGC	180
TGAACGTGTC	GGTGGTGTCT	GAGGAGGTCT	GCAGTAAGCT	CTATGACCCG	CTGT	234

(2) INFORMATION FOR SEQ ID NO:46:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 590 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:

ACTTTTTATT	TAAATGTTTA	TAAGGCAGAT	CTATGAGAAAT	GATAGAAAAC	ATGGTGTGTA	60
ATTGATAGC	AATATTTTGG	AGATTACAGA	GTTTTGTAA	TTACCAATTA	CACAGTTAA	120
AAGAAGATAA	TATATTCCAA	GCANATACAA	AATATCTTA	GAAAGATCAA	GGCAGGAAAAA	180
TGANTATAAC	TAATTGACAA	TGGAAATCA	ATTTTAATGT	GAATTGCAAA	TTATCCCTTA	240
AAAGCTTTC	AAANAAAANAA	TTATTCGAGT	CTANTTAAT	CAAACAGTGT	AAATATGGTAT	300
CAAGGATAAN	AACCTAGGG	CANAAGAAT	TTATTTTAC	TTCATGTAAC	NCACCCANAT	360
TTACAATGGC	TAAATAGTCAN	GGAAAAGCGA	GTGGAAGTAG	GGAAAGTANTC	AAGGTCTTTC	420
TGGTCTCTAA	TCTGCCTTAC	TCTTTCGGTG	TGGCTTTGAT	CCTCTGGAGA	CAGGTGCCAG	480
GGCTCCGTGTT	ATATCCACAA	TTCCCGACGC	AAGATGAAGG	GATGAAAAG	GACACATGCT	540
GCCCTCCCTT	GAGGAGACTT	CATCTCAC TG	GCCAACACTC	AGTCRACATGT		590

(2) INFORMATION FOR SEQ ID NO:47:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 774 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA:

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:47:

ACAAGGGGGC	ATAATGAAGG	AGTGGGGANA	GATTTTAAAG	AAGGAAAAAA	AACGAGGCC	60
TGAACAGAAT	TTTCCTGNAC	AACGGGGCTT	AAAATAATT	TTCTTGGGA	GGTCAAGAC	120

GCTTCACTGC TTGAAACTTA AATGGATGTG GGACANAATT TTCTGTAATG ACCCTGAGG	180
CATTACAGAC GGGACTCTGG GAGGAAGGAT AAACAGAAAAG GGGACAAAAGG CTAATCCCAA	240
AACATCAAAG AAAGGAGGT GCGCTCATAC CTCCCAGCCT ACACAGTTCT CCAGGGCTCT	300
CCTCATCCCT GGAGGACGC AGTGGAGGA CAACTGACCA TGTCCCCAGG CTCCTGTGTC	360
CTGGCTCTG GTCTTCAGCC CCCAGCTCTG GAAGGCCACC CTCTGCTGAT CCTGGCTGGC	420
CCACACTCTT TGAACACACA TCCCCAGGTT ATATTCCTGG ACATGGCTGA ACCTCCTATT	480
CCTACTCCG AGATGCCCTG CTCCCTGCAG CCTGTCAAAA TCCCCACTCAC CCTCCAAACC	540
ACGGCATGGG AAGCCCTTCT GACTGTGCCG ATTACTCCAG CATCTGGAA CAATCCCTGA	600
TCCCCCACTC TTAGSAGCA AGATGGAGTG GTTAAGAGTA GGGCTGGACC ACTTGGAGCC	660
AGGCTGCTGG CTTCAACTTN TGGCTCATT AGCGACTATG GGACCTGGG CAAGTNATCT	720
TCACTTCTAT GGGCNCTCATT TTGTCTACC TGCAAAATGG GGGATAATAA TAGT	774

(2) INFORMATION FOR SEQ ID NO:48:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 124 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:48:

CANAATTGA AATTITATAA AAAGGCATTG TTCTCTTATA TCCATAAAAT GATATAATTG	60
TTGCAANTT ANAAATGTTT CATAAAATTAT AATGTTCTT AATTACAGCT CAACGCAACT	120
TGGT	124

(2) INFORMATION FOR SEQ ID NO:49:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 147 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:49:

GCCGATGCTA CTATTTTATT GCAGGAGGTG GGGGTGTTT TATTATTCTC TCAACAGCTT	60
TGTGGCTACA GGTGGTCTG GACTGCATNA AAAANTTTT TACGGGTGAT TGCAAAAATT	120
TTAGGGCACC CATATCCCAA GCANTGT	147

(2) INFORMATION FOR SEQ ID NO:50:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 107 base pairs
- (B) TYPE: nucleic acid

- (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:50:

ACATTTAAATT AATAAAAGGA CTGTTGGGGT TCTGCTAAAACACATGGCTT GATATATTCG 60
 ATGGTTTGAG GTTAGGAGGA GTTAGGCATA TGTTTGGGA GAGGGGT 107

(2) INFORMATION FOR SEQ ID NO:51:

- (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 204 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:51:

GTCCTAGGAA GTCTAGGGGA CACACGACTC TGGGGTCACG GGGCGGACAC ACTTGCACGG 60
 CGGGAAAGGA AGGCAGAGAA GTGACACCGT CAGGGGGAAA TGACAGAAAG GAAAATCAAG 120
 GCCTTGCAAG GTCAAGAAGG GGACTCAGGG CTTCCACAC ACCCCTGCCCA CACTTGGCCA 180
 CCTCCCCTTT GGACCCACCA ATGT 204

(2) INFORMATION FOR SEQ ID NO:52:

- (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 491 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:52:

ACAAAGATAA CATTATCTT ATAACAAAAA TTGTGATTT TAAAGGTTA GTATTGTGA 60
 GGGTATTTTC CAAAAGACTA AAGAGATAAC TCAGGTAAAA AGTTGAAT GTATAAAACA 120
 CCATCAGACA GGTGTTTAAA AAACACATA TTACAATAAT AGAACATCAT CCTTAAAAAA 180
 AAAACTCTT GTATCAATT CTTTGTCTA AAATGACTGA CTTAANTATT TTAAATATT 240
 TCANAAACAC TTCCCTCAAA ATTTCANA TGGTAGCTT CANATGTNCC CTCAGTCCC 300
 ATGTTGCTA GATAATAAA TCTCGTGA ACTTACACC CACCACAGC TTCTGGGC 360
 ATGCAACAGT GTCTTTCTT TNCTTTCTT TTCTTTTTT TTACAGGCAC AGAAACTCAT 420

CAATTTTATT TGGATAACAA AGGGTCTCCA AATTATATTG AAAATAAAT CCAAGTTAAT
ATCACTCTTG T 480
491

(2) INFORMATION FOR SEQ ID NO:53:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 484 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:53:

ACATAATTA GCAGGGCTAA TTACCATAG ATGCTATTAA TTAANAGGTN TATGATCTGA	60
GTATTAACAG TTGCTGAAGT TTGCTATTAA TATGCAGCAT TTCTCTTTG CTTGATAAAC	120
ACTACAGAAC CCTCTAGAAC ACTGAAAATT AGTAACTAA GTCAGAAAC ATTAGCTGCT	180
CAATCAAATC TCTACATAAC ATCTATGAA TTTAAACGTTT AAAAAGGT GTTGAATCT	240
GCATCTGATAN ANACCGCTCC TGTCAGGATA ANACTGCTTT GGAACAGAAA GGGAAAAAANC	300
AGCTTGTGANT TTCTTTGTGC TGATANGGG AAAGGCTGAA TTACACTTGTG ECCTCTCCCT	360
AATGATTTGGC AGGTCTGGTA AATNCACAAAT CATATCCCA CTCAACACTT CTTTCTCCCT	420
CANTCTGTGATTG CAGGANCAGG CGGATGGAAT GGGCAGGCC NCAGATGTTG	480
	484

(2) INFORMATION FOR SEQ ID NO:54:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 151 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:54:

ACTAAACCTC GTGCTTGTGA ACTCCATACA GAAAACGGTG CCATCCCTGA ACACGGCTGG	60
CCACTGGGTA TACTGCTGAC AACCGCAACA ACAAAAACAC AAATCCTTGG CACTGGCTAG	120
TCTATGTCTT CTCAGTGGC TTTTGTGTTG T	151

(2) INFORMATION FOR SEQ ID NO:55:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 91 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:55:

ACCTGGCTTG TCTCCGGGTG GTTCCCGGCC CCCCCCAGCG TCCCCAGAAC GGACACTTC
GCCCTCCAGT GGATACTCGA GCCAAAGTGG T

60

91

(2) INFORMATION FOR SEQ ID NO:56:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 133 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:56:

GGCGGATGTG CGTTGGTTAT ATACAAATAT GTCATTTAT GTAAGGGACT TGAGTATACT
TGGATTITG GTATCTGTGG GTTGGGGGA CGGTCCAGGA ACCAATAACC CATGGTACCC
AAGGGACAAC TGT

60

120

133

(2) INFORMATION FOR SEQ ID NO:57:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 147 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:57:

ACTCTGGAGA ACCTGAGGCC CTGCTCCGCC TCTGGATGA GTGTGATGCAN GCNGTGCGC
GACTGGGAGC TGAGCCCCTC CCTTTGGGCC TGCCCTCAGAG GATTGTTGCC GACNTGCANA
TCTCANGGG CTGGATNCAT GCAGGGT

60

120

147

(2) INFORMATION FOR SEQ ID NO:58:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 198 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:58:

ACAGGGATAT	AGGTTTNAAG	TTATTGTNAT	TGTAAAATAC	ATTGAATTT	CCTGTATACTC	60
TGATTACATA	CATTATCCCT	TTAAAAAAGA	TGTAAATCTT	ATTTTATG	CCATCTTA	120
ATTTACCAAT	GAGTTACCTT	GTAAATGAGA	AGTCATGATA	GCACGTGATT	TAACTAGTT	180
TTGACTTCTA	AGTTGGT					198

(2) INFORMATION FOR SEQ ID NO:59:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 330 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:59:

ACAACAAATG	GGTTGTGAGG	AAGTCTTATC	AGCAAATCG	GTGATGGCTA	CTGAAAAGAT	60
CCATTGAAAAA	TTATCATTTAA	TGATTTTAA	TGACAAGGT	TCAAAACTC	ACTCAATTTC	120
CACCTGTGCT	AGCTTGCTAA	AATGGGAGT	AACTCTAGAG	CAAATATAGT	ATCTTCTGAA	180
TACAGTCAAT	AAATGACAAA	GCCAGGGCT	ACAGGTGGTT	TCCAGACTT	CCAGACCCAG	240
CAGAAGGAAT	CTATTTTATC	ACATGGATCT	CCGTCTGTG	TCAAAATACC	TAATGATT	300
TTTCGTCTTT	ATTGGACTTC	TTTGAAGAGT				330

(2) INFORMATION FOR SEQ ID NO:60:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 175 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:60:

ACCGGTGGGT	CCTTCTACAT	TCCTGACGGC	TCCTTCACCA	ACATCTGGTT	CTACTTCGGC	60
GTCGTGGGT	CCTTCTCTT	CATCTCATC	CAGCTGGTC	TGCTCATCGA	CTTTGCGCAC	120
TCCTGGAACC	AGCGGTGGC	GGGCAAGGCC	GAGGAGTGCG	ATTCCCGTGC	CTGGT	175

(2) INFORMATION FOR SEQ ID NO:61:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 154 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:61:

ACCCCACTT TCCCTCCGTG AGCAGTCTGG ACTTCTCACT GCTACATGAT GAGGGTGAGT- 60
GGTTGTTGCT CTTCAACAGT ATCCTCCCCCT TTCCGGATCT GCTGAGCCGG ACAGCAGTC 120
TGGACTGCAC AGCCCCGGGG CTCCACATTG CTGT 154

(2) INFORMATION FOR SEQ ID NO:62:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 30 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:62:

CGCTCGAGCC CTATAGTGAG TCGTATTAGA 30

(2) INFORMATION FOR SEQ ID NO:63:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 89 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:63:

ACAAGTCATT TCAGCACCCCT TTGCTCTCA AAACTGACCA TCTTTTATAT TTAATGCTTC 60
CTGTATGAAT AAAAATGGTT ATGTCAAGT 89

(2) INFORMATION FOR SEQ ID NO:64:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 97 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Homo sapiens*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:64:

```

ACCGGAGTAA CTGAGTCGGG ACGCTGAATC TGAATCCACC AATAAATAAA CGTTCTGAG 60
ATCACTGCA TCCAGGATTG GTCTTGATG CTGGGT 97

```

(2) INFORMATION FOR SEQ ID NO:65:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 377 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Homo sapiens*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:65:

```

ACAAACAANAA NTCCCTTCTT TAGGCCACTG ATGGAACACT GGAACCCCT TTTGATGGCA 60
GCATGGCGTC CTAGGCCCTG ACACAGGGC TGCGGTTGG GCTNTCCCAA ACCGCACACC 120
CCAACCCCTGG TCTCTTCCACA NTTCTGGCTA TGCGCTGTCT CTGCCACTGA ACATCAGGGT 180
TCGGTCATAA NATGAAATCC CAANGGGAG AGAGGTCACT AGAGGAAAGCT CAATGAGAAA 240
GGTGCCTTT GCTCAGGCCAG AAAACAGCTG CCTGGCATTC GCCGCTGAAC TATGAACCCG 300
TGGGGGTGAA CTACCCCCCAN GAGGAATCAT GCCTGGGCGA TGCAANGGTG CCAACAGGAG 360
GGCGGGGAGG AGCATGT 377

```

(2) INFORMATION FOR SEQ ID NO:66:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 305 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Homo sapiens*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:66:

```

ACGCCCTTCC CTCAGAACCC AGGGAAGAGA CTGTCGCCCTG CCTTCCTCCG TTGTTGCGTG

```

AGAACCCGTG TGCCCCCTCC CACCATATCC ACCCTCGCTC CATCTTGTAA	120
AGAACCTAAGT TGCACCCCTGG TCCCTCTCCC AGTCCCCAGT TCACCCCTCCA	180
TCCCTCACCT TCCCTCACT TAAGGGATAT CAACACTGCC CAGCACAGGG GGCCTGAATT	240
TATGTGGTTT TTATATATT TTTATAAAGA TGCACTTAT GTCATTTTTT AATAAAAGTCT	300
GAAGAATTAC TGTTT	305

(2) INFORMATION FOR SEQ ID NO:67:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 385 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:67:

ACTACACACA CTCCACTTGC CCTTGTGAGA CACTTTGTCC CAGCACTTAA	60
GGTCGGACCA GCCACATCTC ATGTCAGAAGA TTGCCAGAGA GACATCAGGT	120
CCCTTTAAA AAAGGGGACT TGCTTAAAAA AGAAGTCTAG CCACGATGTTG	180
TGTCGCTGTC TTGGAGATTC CTTTTGAGAG AGTCTCTTC TGAGACCTTG	240
CTGGGAGTC TTGCACATGA GATGGGGCTC GTCTGATCTC AGCAGCTCTT	300
CCTCTCCCAAG GGCCCCAGCC TGGCACACCC TGCTTACAGG GCACCTCTAG	360
CATAGTTCTC GTGCTAGTGG ACCGT	385

(2) INFORMATION FOR SEQ ID NO:68:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 73 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:68:

ACTTAACCAG ATATATTTT ACCCCAGATG GGGATATTCT TTGTAAAAAA TGAAAATAAA	60
GTTTTTTAA TGG	73

(2) INFORMATION FOR SEQ ID NO:69:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 536 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA
 (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Homo sapiens*
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:69:

ACTAGTCCAG TGTGGTGGAA TTCCATTGTC TTGGGGCTC TCACCCCTCT CTCCCTGCAGC	60
TCCAGCTTG TGCTCTGCCG CTGAGGGAGC CATGGCCAG CATCTGAGTA CCTCTGCTGCT-	120
CCTCTGCGC ACCCTAGCTG TGCCCTGGC CTGGACCCC AAGGAGGAGG ATAGGATAAT	180
CCCGGGTGGC ATCTATAACG CAGACCTCAA TGATGAGTGG GTACAGCTG CCTCTCACTT	240
CGCCATCAGC GAGTATAACA AGGCCACAA AGATAGCTAC TAGACAGCTC CGCTGCGGGT	300
ACTAAAGAGCC AGGCCAACAG CGGTGGGGG GTGGAATTAC TTCTTCGAGC TAGAGGTTGG	360
CCGAACCCATA TGATACCAAGT CCCAGCCAA CTTGGACACC TGTGCTCTT ATGAAACAGCC	420
AGAACTGCAG AGAACACAGT TGTGCTCTT CGAGATCTAC GAAGTTCCCT GGGGAGAACAA	480
GAANGTCCTT GGGTGAATC CAGGTGCTAA GAAATCTAN GGATCTGTG CCAGGC	536

(2) INFORMATION FOR SEQ ID NO:70:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 477 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: cDNA
 (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Homo sapiens*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:70:

ATGACCCCCA ACAGGGCCCC TCTCAGCCCT CCTAATGACC TCCGGGCTAG CCATGTGATT	60
TCACTTCCAC TCCATAACCGC TCTCTACTT AGGCCACTA ACCAACACAC TAACCCTATA	120
CCAATGATGC CCCGATGTA CACGAGAAA CACATACCAA GGCCACCCACA CACCCACCTGT	180
CCAAAAAGGC CTTCGATAGC GGATAATCTT ATTATTTACCG TCAGAAGTTT TTTTCTTCGC	240
AGGGATTTT CTGAGCTTTT TACCCATCCA GCCTAGCCCC TACCCCTCAA CTAGGAGGGC	300
ACTGGGCCCC AACAGGCATC ACCCCGCTAA ATCCCTAGA AGTCCCACCT CTAAACACAT	360
CCGTTTACTT CGCATCAGGA GTATCAATCA CCTGAGCTCA CCATAGCTTA ATAGAAAACA	420
ACCGAAACCA AATTATTCAA AGCATGCTT ATTACAAATT TACTGGGTCT CTATTTT	477

(2) INFORMATION FOR SEQ ID NO:71:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 533 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: cDNA
 (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Homo sapiens*
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:71:

AGAGCTATAG	GTACAGTGTG	ATCTCAGCTT	TGCAAACACA	TTTCTACAT	AGATAGTACT	60
AGGTATTAA	AGATATGTAA	AGAAAGAACAT	CACACCATT	ATAATGGTAA	GATTGGTTA	120
TGTGATTAA	GTGGTATTTC	TGGCACCCCT	ATATATGTTT	TCCAACATT	CAGCAGTGAT	180
ATTATTCGA	TAACCTAAA	AGTGAGTTG	AAAAAGAAA	TCTCAGCAA	GCATCTCATT	240
TAATAAAGG	TTTGTCACTT	TTAAAAAATAC	AGCAATATGT	GACTTTTAA	AAAAGCTGTC	300
AAATAGGTG	GACCTACTA	ATAATTATTA	GAATACATT	TAACAAACATC	GAGTACCTCA	360
AGTCAGTTG	CCTTGAAAAA	TATCAAATAT	AACTCTTAGA	GAATGTACA	AAAAAGAATG	420
CTTCGTAA	TTGGAGTANG	AGGTCCCTC	CTCAATTTC	TATTTTAA	AAGTACATGG	480
AAAAAAAAAA	AATTCAACAA	AGTATATAAG	GCTGTAAAT	GAAGAAATTCT	GCC	533

(2) INFORMATION FOR SEQ ID NO:72:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 511 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:72:

TATTACGGAA	AAACACACCA	CATAATTCAA	CTANCAAAGA	ANACTGCTTC	AGGGCGTGT	60
AAATGAAGG	CITCCAGGCA	GTATTATGT	TAAGAACAC	TAAAAGAGGG	ACAAGGCTAA	120
AAGCCGAGG	ATGTCTACAC	TATANCAGGC	GCTATTGTTG	TTGGCTGGAG	GAGCTGTTGGA	180
AAACATGGA	AGATTTGTC	TGGANATGCC	CGTGGCTATT	CCTCATTTGTT	ATTACANAGT	240
GAGGTTCTT	GTGTCGCCAC	TGGTTTGAAG	ACCGCTTCNC	AATAATGATA	GAATAGTACA	300
CACATGAGAA	CTGAAATGGC	CCAAACCCAG	AAAGAAAGCC	CAACTAGATC	CTCAGAANAC	360
GCTCTCTAGG	ACAATAACCG	ATGAGAAGAAA	GATGGCCCTC	TTGTCCCCC	GTCTGTTATG	420
ATTTCTCTTC	ATTGAGCAGNA	NAACCCCTT	CTTCTAACGA	AACNCAGGTG	ATGATGGCNA	480
AAATACACCC	CCTCTTGAAG	NACCNNGGAGG	A			511

(2) INFORMATION FOR SEQ ID NO:73:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 499 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:73:

CACTGGCAGC	ACTGGTCCA	GTACCAAGTAC	CAATAACAGT	GCCAGTGCCA	GTGCCAGCAC	60
CACTGGTGC	TTCACTGCTG	GTGCCAGCCT	GACGCCACT	CTCACATTG	GGCTCTTCCG	120
TGGCTTGT	GGAGCTGGT	CCAGCACCA	TGGCAGCTCT	GGTGCCTGTG	GTTTCTCTTA	180
CAAGTGAGAT	TTTAGATATT	GTAAATCTG	CCAGTCTTC	TCTTCAGACC	AGGGTGCATC	240

67

CTCAGAAACC TACTCAACAC AGCACTCTAG GCAGCCACTA TCAATCAATT GAAGTTGACA 300
 CTCTGCATTA AATCTATTG CCATTTCTGA .AAAAAAAAA .AAAAAAAAGGG CGGCCGCTCG 360
 ANTCTAGAGG GCCCCTTAA ACCGGCTGAT CAGGCTCGAC TGTCGCCTCTC ANTTCGACAGC 420
 CATCTGTGT TTGCCCCCTCC CCCGNTGCTC TCCCTGACCC TGAAAAGTGC CACTCCACT 480
 GTCCCTTCTT AANTAAAAT 499

(2) INFORMATION FOR SEQ ID NO:74:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 537 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:74:

TTTCATAGGA GAACACACTG AGGAGATACT TGAAGAATTG GGATTCAAGCC GCGAAGAGAT 60
 TTTCAGCTT AACTCAGATA AAATCATGTA AAGTAATAAG GTAAAAAGCTA GTCTCTAAC 120
 TCCAGGCCCA CGCTCTAAGT GAATTTGAACT ATGCGATTCA CAGTGTAGAG TAACACATAA 180
 CATTGTATGC ATGGAAACAT GGAGGAACAG TATACAGTG TCCTCACACT CTAAATCAAGA 240
 AAAGAATGAT AGACTCTGAT TCTACAGTGA TGATTGAATT CTAAATAGG TAATCATTAG 300
 GCTCTTGTAT TTATAANACT TTGGGTACIT ATACTAAATG ATGGTAGTTA TACTGCTTC 360
 CAGTTGGCTT GATATTTTTC TTGATATTAA GATTCTTGAC TTATATTG AATGGGTTCT 420
 ACTGAAAAN GAATGATATA TTCTTGAAAGA CTCGATATA CATTATTTA CACTCTTGT 480
 TCTACAATGT AGAAAATGAA GGAATAGGCC CAATATGAT GTTGATAAAA GTCCCGT 537

(2) INFORMATION FOR SEQ ID NO:75:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 467 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:75:

CAAANACAAAT TGTTCAAAGG ATGCAAATGAA TACACTACTG CTGCAGCTCA CAAACACCTC 60
 TGCATATTAC ACGTACCTCC TCCCTGCTCT CAAGTAGTGT GGCTTATTTT GCCATCATCA 120
 CCTGCTGTCT GCTTAGAAGA ACGGCTTCTC GCTGCAANGG AGAGAAATCA TAACAGACGG 180
 TGGCACAAAGG AGGCCATCTT TTCCCTCATCG GTTATTGTC CTAGAACGGT CTTCTGAGGA 240
 TCTAGTTGGG CTTCCTTCTC GGTTTGGGG CATTCTCANTT CTCATGTGTG TACTATTTCTA 300
 TCATTATTTG ATAACGGTT TCAAACNGT GGGCACNCAG AGAACCTCAC TCTGTAAATAA 360
 CAATGAGGAA TAGCCACCGT GATCTCCAGC ACCAAATCTC TCCATGTTNT TCCAGAGCTC 420
 CTCCAGCCAA CCCAAATAGC CGCTGCTATN GTGTAGAACAA TCCCTGN 467

(2) INFORMATION FOR SEQ ID NO:76:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:76:

AAGCTGACAG	CATTGGGGCC	GAGATGTCTC	GTCCTGGC	CTTAGCTGTG	CTCGCGCTAC	60
TCTCTTTT	TGGCTGGAG	GCTATCCAGC	GTACTCCAAA	GATTCAAGGT	TACTCACGTC	120
ATCCAGCAGA	GAATGGAAAG	TCAAATTCTT	TGAATTTGCTA	TGTGCTGCGG	TTTCATCCAT	180
CCGACATTGA	AGTTGACTTA	CTGAAAGATG	GAGAGAGATG	TGAAAAGTG	GAGCATTCAG	240
ACTTGCTTT	CAGCAAGGC	TGGTCTTCT	ATCTCTTGTG	CTACACTGAA	TTCACCCCCA	300
CTGAAAAAGA	TGAGTATGCC	TGCCGTGTGA	ACCATGTCAG	TTGTCACAG	CCCAAGATNG	360
TTNAGTGGGA	TCGANACATG	TAAGCAGCAN	CATGGGAGGT			400

(2) INFORMATION FOR SEQ ID NO:77:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 248 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:77:

CTGGAGTGCC	TTGGTGTTC	AAGCCCTTC	AGGAAGCAGA	ATGACACCTTC	TGAGGCACCT	60
CCAGCTGCC	CGGGGGGGGA	TGCGAGGCTC	GGAGCACCC	TGCCC3GCTG	TGATGCTGC	120
CAGGCACTGT	TCATCTCAGC	TTTCTGTCC	CTTGTCTCC	GGCAAGCCCT	TCTGCTGAAA	180
GTTCATATCT	GGAGCTGTAT	GTCTAACGA	ATAAAGGTCC	CATGCTCCAC	CCGAAAAAAA	240
AAAAAAAAAA						248

(2) INFORMATION FOR SEQ ID NO:78:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 201 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Homo sapiens*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:78:

ACTAGTCCAG	TGTTGGGAA	TTCATTGTG	TTGGGCCAA	CACATGGCT	ACCTTAAAC	60
TCACCCAGAC	CCCGCCCTGC	CCGTGCCCA	CCTGCTGCT	AACGACAGTA	TGATGCTTAC	120
TCTGCTACTC	GGAAACTATT	TTTATGTAAT	TAATGTATGC	TTTCTTGTT	ATAATGCTC	180
GATTTAAAAA	AAAAAAAAAA	A				201

(2). INFORMATION FOR SEQ ID NO:79:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 552 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Homo sapiens*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:79:

TCCTTTGTG	AGGTTTTGA	GACAACCTTA	GACCTAACT	GTGTACAGA	CTTCTGAATG	60
TTAGGCACT	GCTAGTAATT	TCTCTGTAAT	GATTCTGTTA	TTACTTCCT	ATTCTTTATT	120
CCTCTTCCT	CTGAAGATTA	ATGAAGTGA	AAATTGAGGT	GGATAAATAC	AAAAAGGTAG	180
TGTGATGTA	TAAGTATCTA	AGTCAGATG	AAAGTGTGT	ATATATATCC	ATTCAAAATT	240
ATGCAAGTTA	GTAATTACTC	GGATTTAACT	AAATTACTTT	AATATGCTGT	TGACCTACT	300
CTGTTCTTG	GCTAAAAAA	ATTAAACAA	GGACTTGTGTT	AGTTGGGAA	GCCAAATTTGA	360
TAATATTCTA	TGTTCTAAA	GTTGGGTAT	ACATAAANTA	TNAAGAATA	TGGAATTTTA	420
TTCCCAGGAA	TATGGGTTTC	ATTTATGAAT	ANTACCCGGG	ANAGAAGTTT	TGANTNAAAC	480
CNGTTTTGGT	TAATACGTTA	ATATGTCTT	AATNAACAAG	GCNTGACTT	TTTCCAAAAAA	540
AAAAAAAAAA	AA					552

(2). INFORMATION FOR SEQ ID NO:80:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 476 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Homo sapiens*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:80:

ACAGGGATTG	GAGATGCTAA	GGCCCCAGAG	ATCGTTGTG	CCAAACCTCT	TATTTTCAGA	60
GGGGAAAATG	GGGCTTAGAA	GTTACAGAGC	ATCTAGCTGG	TCCGCTGGCA	CCCCCTGGCT	120
CACACAGACT	CCCGAGTAGC	TGGGACTACA	GGCACACAGT	CACTGAAGCA	GGCCCTGTGTT	180
GCAATTCACTG	TGCCCCACTC	CAACTAAC	ATCTTCATA	TGTGATGTCC	TTAGTCACTA	240
AGGTAAACT	TTCCCACCCA	AAAAGGCAA	CTTAGATAAA	ATCTTAGAGT	ACTTTCATAC	300

TCTTCTAAGT CCTCTTCAG CCTCACTTTG AGTCCTCCTT GGGGGTTGAT AGGAANTNTC
 TCTMGGCTTT CTCATAAAA TCTCTATCCA TCTCATGTTT AATTGGTAC GCNTAAAAAT
 GCTGAAAAAA TTAAAATGTT CTGGTTCNc TTAAAAAAA AAAA AAAAAA 360
 420
 476

(2) INFORMATION FOR SEQ ID NO:81:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 232 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:81:

TTTTTTTTTG TATGCCNTCN CTGTGGNGTT ATTGTGGTGTG CCACCCCTGGA GGAGCCCCAGT
 TTCTTCTGTA TCTTTCTTTT CTGGGGATC TTCCCTGGCTC TGCCCCCTCCA TTCCCCAGCT
 TTCCATCCCCA TCTTGCACTT TTGCTAGGGT TGAGGGCGT TTCCCTGGTAG CCCCTCAGAG
 ACTCAGTCAG CGGGAAATAAG TCCTAGGGT GGGGGGTGTG GCAAGCCGGC CT 60
 120
 180
 232

(2) INFORMATION FOR SEQ ID NO:82:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 383 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:82:

AGGCAGGGAG AGAAGCTAAA GCCAAAGCCC AAGAAGAGTG GCAGTGGCAG CACTGGGTG
 AGTACCAAGTA CCAATAAACAT GCGCAAGGCCA GTGCCAGGCC CAGTGGTGCG TTCAGTGTG
 GTGCCAGCCT GACCCGCACT CTCACATTTG GGCTCTTCGC TGGCTTGTG GGAGCTGGTG 60
 120
 180
 240
 CCAGCACCAAG TGCGAGCTCT GTGCGCTGTG GTTCTCTCTA CAAGTGAGAT TTTAGATATT
 GTTAATCTG CCAGTCCTTC TCTTCAAGCC AGGGTGCACTC CTCAAGAAC TACTCAACAC 300
 AGCACTCTNG GCAGCCACTA TCAATCATT GAAGTTGACA CTCTGCATTA AATCTATTG
 CCATTCAA AAAAAAAA AAA 360
 383

(2) INFORMATION FOR SEQ ID NO:83:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 494 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:83:

ACCGAATTGG GACCGCTGGC TTATAAGCGA TCATGTCCTC CAGTATTACC TCAACGAGCA	60
GGGAGATCGA GTCTATACGC TGAAAGAATT TGACCCGATG GGACAACAGA CCTGCTCAGC	120
CCATCCTGCT CGGTTCTCCC CAGATGACAA ATATCTCGA CACCGAATCA CCATCAAGAA	180
ACGCTTCAGG TGCTCTGATG CCCAGAACCC GCGCCCTGTC CTCTGAGGGT CCTTAAACTG	240
ATGCTTTTC TGCCACCTGT TACCCCTCGG AGACTCGCTA ACCAAACTCT TCGGACTGTG	300
AGCCCTGATG CCTTTTTCG AGCCCATACTC TTGGCNCTCT AGTCTCTCGT GGGGATTGTG	360
TATGCTTGTC TGAGGCAATC ATGGTGGCAT CACCCATNAA GGGAAACACAT TTGANTTTT	420
TTTNCATAT TTAAATTAC NACCGAATA NTTCAAGATA AATGAATTGA AAAACTCTTA	480
AAAAAAAAAAA AAAA	494

(2) INFORMATION FOR SEQ ID NO:84:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 380 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:84:

GCTGGTAGCC TATGGCTGG CCACGGANGG GCTCTGAGG CACGGGACAG TGACTTCCA	60
AGTATCCCTGC GCCCGCTCTT CTACCGTCCC TACCTCGAGA TCTTCGGGA GATTCCCGAG	120
GAGGACATGG ACGGGGCCCT CATGGGAGAC AGCAACTGCT CGTGGAGGCC CGGGCTCTGG	180
GCACACCTCT CTGGGGCCCA GGGGGGACCC TGGCTCTCCC AGTATGCCAA CTGGCTGGTG	240
GTGCTGCTCC TCGTCATCTT CTCGCTCGT GCACCAATCC TCTGTCATTG TTGCTCATCG	300
CCATGTTCAAG TTACACATCC GGCACAAAGTAC AGGGCAACAG CNATCTCTAC TGGGAAGGCC	360
AGGGCTTNCCTT CCTCATCCGG	380

(2) INFORMATION FOR SEQ ID NO:85:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 481 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:85:

GAGTTAGCTC	CTCCACAAAC	TTGATGAGGT	CGTCTGCAGT	GGCCTCTCGC	TTCATACCGC	60
TNCATCGTC	ATACTGTAGG	TTGCCACCA	CCTCCATCAT	CTTGGGGCGG	CTAATATCCA	120
GGAAACTCTC	AATCAAGTC	CCGTCNATNA	AACTGTGGC	TGTTTCTGTC	TTCCGCTCGG	180
TGTGAAAGGA	TCTCCAGAAC	GAGTGCTCGA	TCTCCCCAC	ACTTTTGATG	ACTTTATTG	240
GTCGATTCTG	CATGTCAGC	AGGAGGTGT	ACCACTCTC	TGACAGTGAG	GTCACCGGCC	300
CTATCATGCC	NTTGAACTGT	CCGAAGACAA	CCGAGCTTG	TGTTGGGGGT	GNAGTCTCAC	360
CCAGATTCTG	CATTACCAAGA	NAGCGTGGC	AAAAGANATT	GACAACCTGC	CCAGGNNGAA	420
AAAGAACACC	TCCTGAACT	GCTNGCCCT	CCTCGTCCT	TGGTGGNNNC	GCNTNCCTT	480
T						481

(2) INFORMATION FOR SEQ ID NO:86:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 472 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Homo sapiens*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:86:

ACACATCTTCC	TGTATAATGC	TGTGTAATAT	CGATCCGATN	TGTTCTGCTG	AGAATTCTATT	60
ACTTGGAAA	GCAACTTGG	GCGCTGACAC	TGGTATTAAAT	ATTCACAAATA	TGCAACACATT	120
TAACAGTGT	GTCATCTGC	TCCCTTACTT	TGTCATCACC	AGTCTGGAA	TAAGGGTATG	180
CCCTATTCTAC	ACCTGTTAAC	AGGGCGCTAA	GCATTTTGA	TTCAACATCT	TTTTTTTGA	240
CACAGTCGG	AAAATGACAA	AAAGTAAACAG	TTTTAATTT	GTAGGCCAT	TCACTTCTT	300
CATGGGACAG	AGCCATTGGA	TTTAAAGAC	AAATTGCATA	ATATTGAGCT	TTGGGAGCTG	360
ATATNTGAGC	GGAAAGANTAG	CCTTTCTACT	TCACCGACAA	CAACTCCTT	CATATTGGGA	420
GTGTTNACNA	AGTTATGTCT	CTTACAGATG	GGATGCTTT	GTGGCAATTC	TG	472

(2) INFORMATION FOR SEQ ID NO:87:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 413 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Homo sapiens*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:87:

AGAAACCACT	ATCTCTNAAA	ACACCTCTC	ATACCTTGTG	GACCTAAATT	TGTTGCGCTG	60
TGTGTCGCG	CGCATATAT	ATAGACGCC	ACATCTTTT	TACTTTTGT	AAAGCTTAAAG	120
CCTCTTGTG	ATCTATATCT	GTGAAAGGT	TAATGATCTG	CCATAATGTC	TTGGGGACCT	180
TTGCTCTCTG	TGTAATGGT	ACTAGAGAAA	ACACCTATNT	TATGATCTAA	TCTAGTNGT	240
TTTATTCCAC	ATGAAGGAAA	TTCCAGATN	ACAACACTNA	CAAACCTCC	CTTGACTTAG	300
GGGGACAAAG	AAAAGCANA	CTGAACATNA	GAACAAATTN	CCTGGTGAGA	AAATTNCATAA	360

ACAGAAAATTG GGTNGTATAT TGAAANANG CATCATTNAA ACGTTTTTT TTT 413

(2) INFORMATION FOR SEQ ID NO:88:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 448 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA

- (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:88:

CCGAGGGGGT CCTCTCTATC TAGCTCCAGC CTCTCGCTG CCCCACCTCC CGCGTCGCCG	60
GTCCTAGCCN ACCATGGCCG GCCCCCTGG CGCCCCGCTG CTCCCTGCTGG CCATCCCTGGC	120
CGTGGCCCTG CGCCCTGAGCC CGCGGCCCGG CTCCAGTCCC GGCAAGCCGC CGGCCCTGGT	180
GGGAGGCCCCA TGAGCCCCCG GTGGAAGAG AAGGTGTCGG CGCTGCACTG GACTTTGGCCG	240
TCCGGCNANTA CAACAAACCC GCAACACTT TTACCCNAGCN CGGCCCTGAG GTTGTGCCGC	300
CCCAANCAAA TTGTCTACTG GGGTAANTAA TTCTTGAAAG TTGAACCTGG GCCAAACNNG	360
TTTACCCAGA CCNAGCCAT TNGAACATT NCCCTCCAT AACAGCCCCCT TTTAAAAAGG	420
GAANCANTCC TGNTCTTTTC CAAATTIT	448

(2) INFORMATION FOR SEQ ID NO:89:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 463 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA

- (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:89:

GAATTTTGTG CACTGGCAC TGTGATGGAA CCATTGGCC AGGATGCTTT GAGTTTATCA	60
GTAGTGATTG TGCCAAAGTT GGTGTTGATA CATGAGTAG TAAATGCTA AAAAATTAGC	120
AGAGGTCTAG GTCTGCATAT CAGCAGACAG TTGTCCGTG TATTTTGATG CCTTGAAAGT	180
CTCAGTGACA AGTTNNTTCT GATGCGAAGT TCTNATTCGA GIGTTTTAGT CCTTTGCACTC	240
TTTNATGTTN AGACTTGCTT CTNTAAAATT GCTTTGTNT TCTGAGGTA CTATCTGTTG	300
TTTAACAAAA TAGAANNACT TCTCTGCTT GAANATTGAA ATATCTTACA TCTNAAAATN	360
AATTCTCTCC CCATANAAA ACCCANGCCC TTGGGANAAT TTGAAAANG GNTCTTCNN	420
AATTCCNNANA ANTTCAGNTN TCATACAACA NAACNGGNC CCC	463

(2) INFORMATION FOR SEQ ID NO:90:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 400 base pairs
 - (B) TYPE: nucleic acid

- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Homo sapiens*
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:90:

AGGGATTGAA GGTCTNTTNT ACTGTCGGAC TGGTCANCCA CCAACTCTAC AAGTTGCTGT	60
CTTCCACTCA CTGTCGTAA GCNTNTTAAC CCAGACTGTA TCTTCATAAA TAGAACAAAT	120
TCTTCACCGC TCACATCTC TAGGACCTTG TTGGATTCTC TTAGTATAAG CTCTTCCACT	180
TCCTTTGTAA AGACTCTCATC TGTTAAAGTC TTAAAGTTTG TAGAAAGGAA TTAAATGCT	240
CGTTCTCTAA CAATGTCTC TCTTGAAGT ATTTGGCTGA, ACACACCACC TNAAGTCCCT	300
TTGTGCATCC ATTTAAATA TACTTAATAG GGCAATTGGTN CACTAGTTA AATTCTGCAA	360
GAGTCATCTG TCTGCAAAG TTGCGTTAGT ATATCTGCCA	400

(2) INFORMATION FOR SEQ ID NO:91:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 480 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Homo sapiens*
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:91:

GAGCTCGGAT CCAATAATCTT TTGTCGTGAGG GCAGCACACA TATNCAGTGC CATGGNAACT	60
GCTCTACCCC ACATGGGAGC AGCATGCCGT AGNTATATAA GGTCAATTCCC TGAGTCAGAC	120
ATGCCCTCTT GACTACCGTG TGCCAGTGCT GGTGATTCTC ACACACCTCC NNCCGCTTT	180
TGTGAAAAAA CTGGCACTTG NCTGGAACTA GCAAGACATC ACTTACAAT TCACCCACGA	240
GACACTTGAA AGGTGTAAACA AAGCGACTCT TGCAATTGGTT TTGTGCTCTC CGGCACCACT	300
TGTCAATACT AACCCGCTCG TTTGCTCCA TCACATTGTGATCTGTAAGC TCTGGATACA	360
TCTCCGTGACA GTACTGAAGA ATCTTCCTCTT TTGTTTCAAAGCAACTCTT GGTGCGTGT	420
NGATCAGTT CCCATTCCCC AGTCGGATG TTCACATGGC ATATNTTACT TCCCACAAAA	480

(2) INFORMATION FOR SEQ ID NO:92:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 477 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Homo sapiens*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:92:

ATACAGGCCA	NATCCCACCA	CGAAGATGCG	CTTGTGACT	GAGAACTGA	TGCGGTACT	60
GGTCCCGTG	TAGCCCCAGC	GACTCTCCAC	CTGCTGGAA	CGGTTGATGC	TGCACTCCCT	120
CCACGCGG	CAGCAGCGG	GGCCGGTCAAT	GAACCTCACT	CTGGCTTGG	GGTTGACCGGT	180
TAANTGCAGG	AAGAGGTGTA	CCACCTCGCC	GTCCACCAAGG	ATGGCCGACT	GTGCGGGGACC	240
TGCAAGGAAA	CTTCTCGATA	GTCATGAGCG	GGAAAGGGAAT	GANGCCCAGG	GCCTTCGCCA	300
GAACCTTCGG	CTCTGTTCT	GGCGTCACCT	GCAGCTGCG	CGGCTNACAC	TGCGCTCCCG	360
ACCAGCGGAC	AAACGGGTT	GAACACCCGC	ACCTCACGG	TGCCANTGT	GTGCGCTCC	420
AGGAACGGCN	CCAGCGTGT	CAGGTCAATG	TCGGTGAANC	CTCCGCGGGT	AATGGGG	477

(2) INFORMATION FOR SEQ ID NO:93:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 377 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:93:

GAACCGCTGG	ACCTTGCCCT	GCATTGTGCT	GCTGGCAGGA	ATACCTTGGC	AAAGCAGCTCC	60
AGTCGGAGCA	GGCCCGAACCC	AGTGGCCCGCC	GAAGCTAAGC	CTGCGCTCTGG	CCTTCCCTC	120
CGCTCTAACG	CAAGACCAANT	AGTGGAGACA	CTGTGTTAG	AGTTAAAGAGT	GAACACTGGT	180
TGATTTTACT	TGGGAATTTC	CTCTGTTATA	TAGCTTTTC	CAATGCTTAAT	TTCCAACCAA	240
CAAAACAAAA	ATAACATGTT	TGCGCTTNTA	GTGTTATAAA	AGTANTGTAT	TCTGTATNTA	300
AAGAAATAT	TACTGTACA	TATACGTCTT	GCAANTCTG	TATTITATGG	TNCTCTGGAA	360
ATAAAATATAT	TATTTAA					377

(2) INFORMATION FOR SEQ ID NO:94:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 495 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:94:

CCCTTTGAGG	GGTTAGGGTC	CAGTCCCG	TGGAAAGAAC	AGGCCAGGAG	AANTGCGTGC	60
CGAGCGTGG	CAGATTTC	ACAGTGA	CAGAGCC	GGCTATAGTC	TCTGACCCCT	120
CCAAGGAAAG	ACCACCTT	GGGGACATGG	GCTGGAGGC	AGGACCTAGA	GGCACCAAGG	180
GAAGGGCCCA	TTCCGGGGCT	GTTCCTCGAG	GAGGAAGGG	AGGGGCTCG	TGTGCCCCCC	240
ACGAGGAANA	GGCCCTGANT	CCTGGGATCA	NACACCCCT	CACGTGTATC	CCACACACAA	300

TGCAAGCTCA CCAAGGTCCC CTCTCAGTCC CTTCCCTACA CCCTGAACGG NCACTGGCCC	360
ACACCCACCC AGANCANCCA CCCGCCATGG GGAATGTNCT CAAGGAATCG CNGGGCAACG	420
TGGACTCTNG TCCCNNAAGG GGGCAGAATC TCCAATAGAN GGANNGAAC CTTGCTNANA	480
AAAAAAAAAA AAAA	495

(2) INFORMATION FOR SEQ ID NO:95:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 472 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:95:

GGTTACTTGG TTTCATTGCG ACCACTTAGT GGATGTCAATT TAGAACCATTT TTGCTGTGTC	60
CCTCTGGAAAG CCTTGCAG ACGGGACTTTT GTAAATTGTTG GAGAAACTT GCTGAATT	120
TAGCTGTTT GAGTTGATTC GCACCACTGC ACCACAACCT AATATGAAAAA CTATTTNACT	180
TATTTATAT TTGATGAAAAA GTATACAATG AAAATTGTTG CTACATGTA TTTATCAAGT	240
ATGATGAAAAA GCAATAGATA TATATTCTT TATTATGTTT TATTATGATT GCCATTATTA	300
ATCGGCAAAA TGTGGAGTGT ATGTTCTTTT CACAGTAATA TATGCCTTTT GTAACCTCAC	360
TTGGTTATT TATTGTAAT GAATTACAAA ATTCCTTAATT TAAGAAAATG GTANGTATA	420
TTTANTTCAN TAATTCCTTT CCTTGTTAC GTTAATTGTTG AAAAGAACATC AT	472

(2) INFORMATION FOR SEQ ID NO:96:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 476 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:96:

CTGAAGCATT TCTTCAAAC TNTCTACTTT TGTCATTGAT ACCTGTAGTA AGTTGACAAAT	60
GTGGTGAATAT TTCAAATTAA TATGTAACCTT CTACTAGTTT TACTTTCTCC CCCAAGTCTT	120
TTTTAACTCA TGATTTTAC ACACACAACTC CAGAACCTTAT TATATAGCTT CTAAGTCTTT	180
ATTCCTCACA TGAGATGATG AAAGAGCTCT CGAGTGTCTT GNCGCANAAATG TTCTAGNTAT	240
AGCTGGATAC ATACANGTGGG AGTTCTATAA ACTCATACCT CAGTGGGACT NAACCAAAT	300
TGTGTTAGTC TCAATTCTCA CCACACTGAG GGAGGCTCCC AAATCCTAT ATTCTTATCT	360
GCAGGGTACTC CTCCAGAAAA ACNGACAGGG CAGGCTGTCA TGAAAAGTIN ACATCTGGCT	420
TACAAAGTCT ATCTTCTCA NANGTGTGN AAGGAACAT AATATCTT AGCTTT	476

(2) INFORMATION FOR SEQ ID NO:97:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 479 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:97:

```

ACTCTTCTA ATGCTGATAT GATCTTGAGT ATAAGAACATG ATATGTCACT AGAAATGGATA    60
AAATAATGCT GCAAACCTAA TGTCTTCTAT CAAATGGAA CGCTAAATGAA ACACAGCTTA 120
CAATCGAAA. TCAAAACTCA CAAGTGCCTA TCTGTTGATG ATTATGTTAA ATAAGCTTA 180
GATTGTCCTC CTTCGGATG GATTGTTCT CANATCTTGG GCAATNTTCC TTAGTCAAAT 240
CAGGCTACTA GAATTCGTGTT ATTGGATATN TGAGAGCATG AAATTTTAA NAATACACTT 300
GTGATTATNA AATTAATCAC AAATTTCACT TATACCTGTT ATCACGACT AGAAAAACAT 360
NTNNNTTTTA NATCAAAGT TTTTGTGTTT GGAANTGTNN AAATGAAATC TGAAATGTTG 420
TTCNATCTTA TTTTCTCCN GACNACTANT TNCCTTTTTA GGNCTTATTC TGANCCATC 479

```

(2) INFORMATION FOR SEQ ID NO:98:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 461 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:98:

```

AGTGACTTGT CCTCCAACAA AACCCCTTGA TCAAGTTGT GGCACTGACA ATCAGACCTA    60
TGCTAGTTCC TGTCTATCAT TCGCTACTAA ATGCAGACTG GAGGGGACCA AAAAGGGGCA 120
TCAACTCCAG CTGGATTATT TTGGAGCTCG CAAATCTATT CCTACTTGTG CGGACTTTGA 180
AGTGATTCTG TTTCTCTAC GGATGAGACA CTGGCTCAAG AATATCTCA TGCACTTTA 240
TGAAGCCACT CTGAACACCG TGGTTATCTA GATGAGAAACA GAGAAATAAA GTCAAGAAAAT 300
TTAACCTGGG AAAAGAGGGT TTGGCTGGG ACCATCCCAT TGAACTTCTT CTTAAGGACT 360
TTAAGAAAAA CTACCCACAT TTGTGTATCC TTGTGCGGGC CGTTTATGAA CTGACCACCC 420
TTTGGAAATAA TCTTGACGCT CCTGAACCTG CTCCTCTGGC A 461

```

(2) INFORMATION FOR SEQ ID NO:99:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 171 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:99:

GTGGCCGCGC GCAGGTGTTT CCTCGTACCG CAGGGCCCCC TCCCTTCCCC AGGCCTCCCT	60
CGGGCCTCT CGGGCCCGA GGAGGAGCGG CTGGCGGTG GGGGGAGTGT GACCCACCC	120
CGGGAGAAA AGCCTTCTCT AGCGATCTGA GAGGGCTGCC TTGGGGTAC C	171

(2) INFORMATION FOR SEQ ID NO:100:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 269 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:100:

CGCCGCGAAC TGCAACTCCA GCTGGGGCCG TGCGGACGAA GATTCTGCCA GCAGTTGGTC	60
CGACTCGCAC GACGGCGGG GCGACAGTCG CAGTCGCGAC CGCGGGCCCT GGGGTCTTGC	120
AAGGCTGAGC TGACGCCGA GAGGTCGTGT CACGTCACAG GACCTTGACG CGCTCGGGGA	180
CAGCCGGAAC AGAGCCCGGT GAAGCGGGAG GCCTCGGGGA GCGCCCTGGG AAGGGCGGGC	240
CGAGAGATAC GCAGGTGCG GTGGCGCC	269

(2) INFORMATION FOR SEQ ID NO:101:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 405 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:101:

TTTTTTTTTT TTTTGGAATC TACTGCAGGC ACAGCAGGTC AGCAACAAAGT TTATTTTGCA	60
GCTAGCAAGG TAACAGGTA GGGCATGGTT ACATGTTCTG GTCAACTTCC TTGTCTGTTG	120
TITGATTGGTT TGTCTTTATG GGGCGGGGT GGGGTAGGG AAACGAAGCA ATAACACTTC	180
AGTGGGTTGC CCCCCTCTGT AGAACCTGGT TACAATGCTT GGGGCAGTTC ACCTGGTCTG	240
TGACCTCGAT TTTCATGACA TCAATGCTG TAAAGTCAG GATATCTTT AGAGAGTCCA	300
CTGTTCTGGA GGGAGATAG GTTCTCTTC CAAATCCAC AAAATCCACT GAAAAAGTTG	360
GATGATCAGT ACGAATACCG AGGCATATTTC TCATATCGGT GGCCA	405

(2) INFORMATION FOR SEQ ID NO:102:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 470 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:102:

```
TTTTTTTTTT TTTTTTTTTT TTTTTTTTTT TTTTTTTTTT TTTTTTTTTT 60
GGCACTTAT CCATTITTTAT TTCAAAATGT CTACAAATTTT AATCCCATTA TAGGTTATTT
TCAAAATCTA AATTATTCAA ATTAGCCAA TCCCTTACCAA ATAATACCCA AAAATCAAAA 120
ATAATCTCT TTCAAGCAACAA TTGTTACATA AATTTAAAAAA ATATATACCG CTGGTGTTTT
CAAAGTACAA TTATCTTAAC ACTGCAACA TTTTAAGGAA CTAAATTTAA AAAAACACT 240
CCGCAAGGT TAAAGGGAAC ACAAATCTC TTACAAACAC CATTATAAAA ATCATATCTC 300
AAATCTTAGG GGAATATATA CTTCACACCG GATCTTAACT TTACTCTACT TGTGTTAATT 360
TTTTAAACCA TTGTTTGCCC CCAACACAA GGAATCCCCC CTGGACTAGT 420
470
```

(2) INFORMATION FOR SEQ ID NO:103:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 581 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:103:

```
TTTTTTTTTT TTTTTTTTGA CCCCCCTCTT ATAAAAAACCA AGTTACCAATT TTATTTTACT 60
TACACATATT TATTTTATAA TTGGTTAG ATATTCAAA GGCACTTTT AAAATCAAC 120
TAAATGGAAA CTGCTTAGA TACATACTT TTAGGAATTG CTTTAAATC TGCTTAAAGT
GAAAATCTC TCTAGCTCTT TTGACTGTAA ATTTTTGACT CTTGAAACAC ATCCAAATTC 180
ATTTTTCTG TCTTTAAATAT TATCTTAATCT TTCCATTTTT TCCCTTATCC AAGTCAAATT 240
GCTTCTCTAG CCTCATTCTTCTAGCTCTTAT CTACTATTAG TAAGTGGCTT TTTTCTAA 300
AGGGAAACAA GGAAGAGAAA TGCGCACACCA AACAAACATT TTATATTCTAT ATTTCCTACCT 360
ACGTTAAATA AATAGCAATT TTGTGAGGCCA GCTCAAAAGA AGGCTTAGAT CCTTTTATGT 420
CCATTCTAGT CACTAAACCGA TATCAAAGTG CCAGAATGCA AAAGGTTTGT GAACATTTAT 480
TCAAAAGCTA ATATAAGATA TTTCACATAC TCATCTTTCT G 540
581
```

(2) INFORMATION FOR SEQ ID NO:104:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 578 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:104:

TTTTTTTTT	TTTTTTTTT	TTTTCTCT	CTTTTTTTT	GAAATGAGGA	TCGAGTTTTT	60
CACTCTCTAG	ATAGGGCATG	AAGAAAACCT	ATCTTCCAG	CTTTAAAATA	ACAATCAAT	120
CTCTTATGCT	ATATCATATT	TTAAGTAA	CTAATGAGCT	ACTGGCTTAT	CTTCTCCCTGA	180
AGGAAATCTG	TTCATCTTC	TCATTCTAT	AGTTATATCA	AGTACTACCT	TGCATATTGA	240
GAGGGTTTC	TTCTTATTT	ACACATATAT	TTCCATGTGA	ATTTGTATCA	AACCTTTATT	300
TTCATGCCAA	CTGAAAGATA	ATGTTTCTT	TGCATAAGGA	AAGAGAACAA	TATAGCATTA	360
CAAAGCTGCT	CAAATTTGTTT	GTAAAGTAT	CCATTATAAT	TAGTTGGCAG	GAGCTAATAC	420
AAATCACATT	TACGACAGCA	ATATAAAAAC	TGAAGTACCA	GTAAATATC	CAAATAATT	480
AAAGGAACAT	TTTTAGCCCG	GGTATAATT	GCTAATTAC	TTTACAAGCA	TTTATTAGAA	540
TGAATTACA	TGTTTATTATT	CCTAGCCCCA	CACAATGG			578

(2) INFORMATION FOR SEQ ID NO:105:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 538 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:105:

TTTTTTCTAGT	ATAATCAGAA	CAATATTAT	TTTTTATTTT	AAAATTCTATA	60	
GAAAAGTGCC	TTACATTAA	AAAAGTTTG	TTTCTCAAG	TGATCAGAGG	AATTAGATAT	120
GTCTTGAACA	CCAATATTA	TTTGAGGAAA	ATACACCAA	ATACATTAA	TAATTTTATTT	180
AAGATCATAG	AGCTTGTAG	TGAAAGATA	AAATITGACC	TCAGAAACTC	TGAGCATTA	240
AAATCCCTAA	TTAGCAATA	AATTACTATG	GACTTCTTG	TTAATTTTG	TGATGAAATA	300
GGGGTGTCA	TGGTAAACCA	ACACATCTG	AAGGATACAT	TACTTGTGA	TAGATTCTTA	360
TGTACTTGC	TAATACGTGG	ATATGAGTTG	ACAAAGTTCT	CTTCTCTCAA	TCTTTTAAGG	420
GGCGAGAAAT	GAGGAAAGAA	AGGAAAGGAT	TACGCATACT	GTTCCTTCTA	TGGAAGGATT	480
AGATATGTTT	CTCTTGCCAA	TATTAAGAAA	ATATAATGT	TTACTAATAG	TGAAACCC	538

(2) INFORMATION FOR SEQ ID NO:106:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 473 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:106:

TTTTTTTTTT	TTTTTTAGTC	AAAGTTCTAT	TTTTATATATA	-ATTAAAGTCT	TGGTCATTC	60
ATTTATTAAGC	TCTGCAACT	ACATATTAA	ATTAAGAAA	CGTTTAGAC	AACGTACAA	120
TTTATAAATG	TAAGGTGCCA	TTATGAGTA	ATATATCCT	CCAAGAGTGG	ATGTGTCCT	180
TCTCCACCA	ACTAATGAAC	ACCAACATTA	GTTTANTTTT	ATAGTAGAT	ATACACTGCT	240
GCAAACGCTA	ATTCTCTCTC	CCATCCCCAT	GTGATATTGT	GTATATGTGT	GAGTTGGTAG	300
AATGCATCAC	AATCTACAAT	CAACAGCTAG	ATGAAGCTAG	GCTGGGCTTT	CGGTGAAAT	360
AGACTGTGTC	TCTTGATGAT	AAATGATCTG	ACCTATCCTC	GTTGGCAAGA	ACTCTCTGAA	420
CCGCTTCCTC	AAAGGCCTG	CCACATTGT	GCCTCTTTC	ACTTGTTC	AAA	473

(2) INFORMATION FOR SEQ ID NO:107:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1621 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:107:

CGCCATGGCA	CTGCAAGGGCA	TCTCGGGTCAT	GGAGCTGTCC	GGCTCTGGCC	CGGCCCGGTT	60
CTGTGCTATG	GTCTCTGGCTG	ACITCGGGGC	CGCTGTGGTA	CGCTGGACCC	GGCCCGGCTC	120
CCGCTACGAC	GTAGGCCGT	TGGGCCGGG	CAACGCCCG	CTAGTGTGG	ACCTGAAGCA	180
GGCCGCGGGG	GCGCCGGTGC	TGGCGCTCT	GTGCAACGGG	TGGCATGTGC	TGCTGGAGCC	240
CTTCGGCGGC	GGTGTCTATGG	AAAGAACCTCA	GCTGGGCCA	GAGATTCCTG	AGCGGGAAAAA	300
TCCAAGGCTT	ATTATATGCCA	GGCTGAGTGT	ATTTGGCCAG	TCCAGGAAGCT	TCTGCGCGTT	360
AGCTGGCCAC	TACACTAAGCT	ATTGGCTTT	GTCAAGGTGT	CTCTCAAAA	TGGCAGAAAG	420
TGGTGAAGATA	CGCTATGCC	CGCTGAATCT	CCTGGCTGAC	TTGCTGGTC	GTGCGCTTAT	480
GTGTGCACTG	GGCATTTATAA	TGGCTCTTCT	TGACCCGCA	CCACACTGACA	AGGGTCAGGT	540
CATTGATGCA	AATAATGTTG	AGAGGAACAGC	ATATTTAAGT	TCTTCTCTG	GGAAAAGTC	600
GAATATCGAGT	CTGTGGGAAG	CACCTCGAGG	TCAGAACATG	TGGATGGTG	GAGCACCTTT	660
CTATACGACT	TACAGGACAG	CAGATGGGGA	ATTCATGGT	GTGAGGCAA	TAGAACCCCA	720
GTTCCTACGAG	CTGCTCATCA	AAGGACTTGG	ACTAAAGCT	GTAGAACATT	CCAATCGAGAT	780
GAGCTATGG	GATTGGCCAG	AAATGAAGAA	GAAGTTTGCA	GTATGTTATG	CAAAGAACAG	840
GAAGGCAGAG	TGGTGTCAAA	TCTTTGACCG	CACAGATGCC	TGTGTGACTC	CGGTCTCTGAC	900
TTTGGAGGA	GTGTGTCATC	ATGATCACAA	CAAGGAACGG	GGCTCTTTA	TCACCCAGTGA	960
GGAGCAGGAG	GTGAGCCCCC	GCCCTGCA	TCTGCTGTTA	AAACCCCG	CCATCCCTTC	1020
TTTCAAAAGG	GATCTTCTTA	TAGGAGAACCA	CACTGAGGAG	ATATTTGAG	ATTGTTGGATT	1080
CAGCCGCGAA	GAGATTTTAC	AGCTTAACTC	AGATAAAATC	ATTGAAAGTA	ATAAGGTAA	1140
AGCTAGTCTC	TAACCTCCAG	GCCCACGGT	CAAGTGAATT	TGAATACTGC	ATTACACTG	1200
TAGAGTAACA	CATAACATG	TATGCTGATG	AAACATGGAGG	AACATGTTA	CAGTGTCTTA	1260
CCACTCTAA	CAAGAAAAGA	ATTACAGACT	CTGATTCAC	AGTGATGATT	GAATTCCTAA	1320
AATGTTTATC	ATTAGGGCTT	TTGATTTATA	AAACTTTGGG	TACTTATACT	AAATTTATGTT	1380
AGTTATTCTG	CCTTCTGAGT	TGCTGTGAT	ATTTGTTGAT	ATTAAGATTC	TTGACTTATA	1440
TTTGAATGG	GTTCTAGTGA	AAAAGGAATG	ATATATTCTT	GAAGACATCG	ATATACATT	1500
ATTTACACTC	TTGATTCTAC	AATGAGAAA	ATGAGGAAT	GCCACAAATT	GTATGGTGAT	1560

AAAAGTCACG TGAAACAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA 1620
 A 1621

(2) INFORMATION FOR SEQ ID NO:108:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 382 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:108:

Met Ala Leu Gln Gly Ile Ser Val Met Glu Leu Ser Gly Leu Ala Pro			
1	5	10	15
Gly Pro Phe Cys Ala Met Val Leu Ala Asp Phe Gly Ala Arg Val Val			
20	25	30	
Arg Val Asp Arg Pro Gly Ser Arg Tyr Asp Val Ser Arg Leu Gly Arg			
35	40	45	
Gly Lys Arg Ser Leu Val Leu Asp Leu Lys Gln Pro Arg Gly Ala Ala			
50	55	60	
Val Leu Arg Arg Leu Cys Lys Arg Ser Asp Val Leu Leu Glu Pro Phe			
65	70	75	80
Arg Arg Gly Val Met Glu Lys Leu Gln Leu Gly Pro Glu Ile Leu Gln			
85	90	95	
Arg Glu Asn Pro Arg Leu Ile Tyr Ala Arg Leu Ser Gly Phe Gly Gln			
100	105	110	
Ser Gly Ser Phe Cys Arg Leu Ala Gly His Asp Ile Asn Tyr Leu Ala			
115	120	125	
Leu Ser Gly Val Leu Ser Lys Ile Gly Arg Ser Gly Glu Asn Pro Tyr			
130	135	140	
Ala Pro Leu Asn Leu Leu Ala Asp Phe Ala Gly Gly Leu Met Cys			
145	150	155	160
Ala Leu Gly Ile Ile Met Ala Leu Phe Asp Arg Thr Arg Thr Asp Lys			
165	170	175	
Gly Gln Val Ile Asp Ala Asn Met Val Glu Gly Thr Ala Tyr Leu Ser			
180	185	190	
Ser Phe Leu Trp Lys Thr Gln Lys Ser Ser Leu Trp Glu Ala Pro Arg			
195	200	205	
Gly Gln Asn Met Leu Asp Gly Ala Pro Phe Tyr Thr Tyr Arg			
210	215	220	
Thr Ala Asp Gly Glu Phe Met Ala Val Gly Ala Ile Glu Pro Gln Phe			
225	230	235	240
Tyr Glu Leu Leu Ile Lys Gly Leu Gly Leu Lys Ser Asp Glu Leu Pro			
245	250	255	
Asn Gln Met Ser Met Asp Asp Trp Pro Glu Met Lys Lys Phe Ala			
260	265	270	
Asp Val Phe Ala Lys Lys Thr Lys Ala Glu Trp Cys Gln Ile Phe Asp			
275	280	285	
Gly Thr Asp Ala Cys Val Thr Pro Val Leu Thr Phe Glu Glu Val Val			

290	295	300
His His Asp His Asn Lys Glu Arg Gly Ser Phe Ile Thr Ser Glu Glu		
305	310	315
Gln Asp Val Ser Pro Arg Pro Ala Pro Leu Leu Leu Asn Thr Pro Ala		320
325	330	335
Ile Pro Ser Phe Lys Arg Asp Pro Phe Ile Gly His Thr Glu Glu		
340	345	350
Ile Leu Glu Phe Gly Phe Ser Arg Glu Glu Ile Tyr Gln Leu Asn		
355	360	365
Ser Asp Lys Ile Ile Glu Ser Asn Lys Val Lys Ala Ser Leu		
370	375	380

(2) INFORMATION FOR SEQ ID NO:109:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1524 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:109:

GGCACGAGGC	TGGCCGAGGG	CCTGAGCGGA	GGCGGGGGCA	GCCTCGCCAG	CGGGGGCCCC	60
GGGCTGGCC	ATGCCCTAC	GAGGCCAGGC	CTGGCCCTCT	ACCTCGCCGA	CAGCTGGAAC	120
CAGTGCACC	TAGTGGCTCT	CACCTGCTC	CTCCCTGGGG	TGGGCTGCCG	GCTGACCCCG	180
GGTTTGATACC	ACCTGGGCGG	CACTGTCCIC	TGCATCGACT	TCTATGGTTT	CACCGTGGCG	240
CTGCTTCACA	TCTTCAGGT	CAAACAAACAG	CTGGGGGCCA	ATGATCGCAT	CGTAGGAAAG	300
ATGATGAGGG	ACGGTGTCTT	CTTCTCTTC	TTCCCTGGGG	TGTGGCTGGT	AGCCTATGGC	360
GTGCCACAGG	AGGGGCTCCT	GAGGCCACGG	GACAGTGACT	TCCCCAGTAT	CTTCCGGCCGC	420
GTCTTCTTAC	GTCTCTTACG	GGCAGATCTC	GGCAGATCTC	CCCAGGAGGA	CATGGACGTG	480
GCCCCATAGG	AGCACACGAA	CTGCTCTCG	GGACCCGGAC	TCTGGGCACA	CCCTCTCTGGG	540
GCCCCAGGGG	GCACCTCGGT	CTTCCAGTAT	GCCAACCTGG	TGGTGGTGTG	GCTCTCTCGTC	600
ATCTTCTTGC	TGCTTCTTAC	CAATCCCTGTC	GTCAACTTGC	TCTATTGCCAT	GTTCACTTAC	660
ACATCTCGCA	AAAGTACAGGG	CTCTACAGGT	TCTACTGGGA	AGGGCAGGG	TTACCCGGCTC	720
ATCCGGGAAT	TCCACTCTCG	GCCCCGGCTG	GGCCCGCCCT	TTATCGTCAT	CTTCCACTTG	780
CGCCCTCTCG	TCAGGGCTAC	GTGCAAGGG	CCCCGGAGCC	CCCAGCGCTC	CTCCCCGGGC	840
CTCGAGGATT	TCTGGGTTTA	CTTCTTAAAG	GRAGGCCGAGC	GGAAAGCTGT	AACGTGGGAA	900
TCGGTGTGATA	AGGAGAACTT	TCTGCTGGCA	CGCGCTAGGG	ACAAAGGGGA	GAGCCACTCC	960
GAGCGTCTGA	AGCGCACGTC	CCAGAGGGTG	GACTTGGCAC	TGAAAACAGCT	GGGACACATC	1020
CGCGAGTAGG	ACACGGCCT	GAAAGTGTG	GAGCGGGAGG	TCCAGCAGTG	TAGCCGGCTC	1080
CTGGGTGAGG	TGGCCGAGGC	CTGAGCCGC	TCTGCTCTGC	TGCCCCCAGG	TGGGCCGCCA	1140
CCCCCTGACC	TGCCCTGGGT	CAAAGACTGA	GCCCCGTGCTG	CGGACTTCAA	GGAGAAAGCCC	1200
CCACAGGGGA	TTTTGCTCTT	AGAGTAAGGC	TCATCTGGG	TCTGGGCCCC	GCACCTGGTG	1260
GCTCTTGCTC	TGAGGTGAGC	CCCATGTCCA	TCTGGGCCAC	TGTCAAGGAC	ACCTTTGGGA	1320
GTGTCACTCT	TACAAACCCAC	AGCATGGCCG	GCTCTCTCCA	GAACCACTTC	CAGCCTGGGA	1380
GGATCAAGGC	CTGGATCCCG	GGCCCTTATC	CATCTGGAGG	CTGCAAGGTC	CTTGGGGTAA	1440
CAGGGACAC	AGACCCCTCA	CCACTCACAG	ATTCTCACCA	CTGGGAAAT	AAAGCCATT	1500
CAGGAGAAAA	AAAAAAA	AAAA				1524

(2) INFORMATION FOR SEQ ID NO:110:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3410 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:110:

GGAAACCCAGC	CTGCACCGCG	TGACCTCCGGG	TGACAGCCGC	GGCCCTCGGC	CAGGATCTGA	60
GTGATGAGAC	GTGCCCCCAC	TGAGGTGCC	CAACAGAGCA	GGTGTGAGC	ATGGGCTGAG	120
AAAGCTGACC	GGCACCAAAG	GGCTGGCAGA	AATGGGCGGC	TGGCTGATT	CTAGGGCTGTT	180
GGCGGCAGCA	AGGAGGAGAC	GGCCGAGCTT	CTGGAGCAGA	CGCGAGACGA	AGCAGTCTCG	240
GAGTGGCTGA	ACGGGCCCCCT	GAGGGCTAAC	GGCCGTGCCC	ACTATGTTCC	AGAGGCTGTG	300
GGTAGAGCCG	CTGCTGCGGC	ACCGGAAGC	CCAGCTCTTG	CTGTCACACC	TGCTAACCTT	360
TGGCTGGAG	GTGTTGTTG	CCCGAGGCA	CACCTATGTC	GGCCCTCTGC	TGCTGGAAAGT	420
GGGGTAGAG	GAGAAGTTCA	TGACCATGGT	GGTGGGCCAT	GGTCAGTGC	TGGGCCCTGGT	480
CTGTTGTC	CTCCTAGGCT	CAGCCAGTGA	CCAATGCGCT	GGACGCTAT	GGCCGGCCCG	540
GCCCTTCATC	TGGGGACTGT	CCTTGGGCAT	CTCTGCTGAGC	CTCTTCTCA	TCCCAAGGGC	600
CGGCTGGCTA	CGAGGGCTGC	TGTTGGCGGA	TCCCAGGCC	CTGGAGCTGG	CACTGTCAT	660
CCTGGGCGTG	GGGCTGCTGG	ACTTCTGTTG	CCAGTGTGTC	TTCACCTCAC	TGGAGGCCCT	720
GCTCTCTGAC	CTCTCCCGG	ACCGGGACCA	CTGTCGCCAG	GGCTACTCTG	TCTATGCTT	780
CATGATCAGT	CTTGGGGCT	GGCTGGCTA	CTCTCTGCC	GGCATTGACT	GGGACACCAAG	840
TGCCCCTGCC	CCCTACCTGG	GCACCCAGGA	GGACTGCTTC	TTTGGCTTC	TCAACCTCAT	900
CTTCTTCACC	TGGCTAGCAG	CCACACTGCT	GGTGGCTGAG	GGGGCAGGGC	TGGGGCCAC	960
CGAGCCAGCA	GAAGGGCTGT	CGGCCCCCTC	CTTGTGCC	CACTGCTGTC	CATGCCGGGC	1020
CCGCTTGGCT	TTCCGGAACC	TGGGGCCCT	GGTCTCCCGG	CTGCACCCAGC	TGTGCTGCCG	1080
CATGGCCCGC	GGCTCTGGCC	GGCTCTCTGT	GGCTAGCTG	TGCACTGGG	TGGCACTCAT	1140
GACCTTCAGG	CTGTTTTACA	CGGATTCTTC	GGGGCAGGGG	CTGTACCAAG	GGGTGCCAG	1200
AGCTGAGCCG	GGCACCGAGG	CCCGGAGACA	CTATGATGAA	GGCCTTCCGA	TGGGCAAGCT	1260
GGGGCTGTT	CTGCTGTGCG	CAATCTCTCT	GGTCTTCTC	CTGGTCATGG	ACCGGGCTGGT	1320
CGACGGATTC	GGCCTACCGAG	CACTGTATTG	GGCAGTGTG	GCAGCTTTC	CTGGGTCTGC	1380
CGGGTCCACA	TGGCTGTCCC	ACAGTGTGTC	CGTGTGACA	GGCTCAGGGG	CCCTCACCCG	1440
GTTCACCTTC	TCAGCCCTGC	AGATCTCTG	CTACACACT	GGCTCTCTT	ACCAACGGGA	1500
GAAGCAGGTG	TTCCCTGCCA	AAATCCGAGG	GGACACTGGA	GGTGTCTAGCA	GTGAGGACAG	1560
CCTGATGACC	AGCTTCTCTG	CAGGCCCTAA	GGCTGGAGCT	CCCTTCTCTA	ATGGACACOT	1620
GGGTGCTGGA	GGCAGTGGCC	TGCTCTCAC	TCCACCCGG	CTCTGGGGG	CCTCTGCC	1680
TGATGTCTC	GTACGTGTGG	TGGTGGGTGA	GGCCACCGAG	GGCAGGGTGG	TTCCGGCC	1740
GGGCATCTGC	CTGGACCTCG	CCATCTGGGA	TAGTGCCTTC	CTGCTGTCCC	AGGTGGCC	1800
ATCCCTGTTT	ATGGGCTCCA	TGTCAGCTG	CAGCGAGTCT	GTCACTGCC	ATATGGTGT	1860
TGCGCAGGG	CTGGGTCTGG	TGGCCATTTC	CTTGTCTACA	CAGGTAGTAT	TTGACAAGAG	1920
CGACTTGGCC	AAATACTCG	CGTAGAACAC	TTCCACACA	TTGGGGTGG	GGGCCCTGCC	1980
CACTCTGGC	CACTCTCCCG	CTCTGTGAG	CCCCATGGGG	CTGCGGGGT	GGCCGCCAGT	2040
TTCTGTGCT	GGCAAAAGTA	TGTTGGCTCT	TCTGTGCC	CTGTGCTGCT	GAGGTGGCTA	2100
GCTGCACAGC	TGGGGGTG	GGCGTCCTC	TCTCTCTCC	CCAGTCTCTA	GGGCTCCTG	2160
ACTGGAGGG	TTCCAGGGG	GTTCTGCTT	GGATTTATAC	AGGGAGGCCA	GAAGGCTCC	2220
ATGCACTGGA	ATGGGGGAC	TCTGCAAGGTG	GATTACCCAG	GTCAGGGTT	AAACAGCTAGC	2280
CTCCTAGTTG	AGACACACCT	AGAGAAGGGT	TTTGGGAGC	TGAATAACT	CACTGCTCTG	2340
GTTCCTCAC	TCTAAGGCC	TTAACCTGCA	GCTTCGTTA	ATGTAACCT	TGATGGGAG	2400
TTCTTAGGAT	GAACACTCC	TCCATGGGT	TTGAACATAT	GACTTATTG	TAGGGGAAGA	2460

GTCCTGAGGG	GCAACACACA	AGAACCCAGGT	CCCCCTCAGCC	CACAGCACTG	TCTTTTTGCT	2520
GATCCCCACCC	CCTCTTACTT	TTTATCAGGA	TGTTGGCTGT	TGGTCCTCT	GTTGCCATCA	2580
CAGACAGACA	GGCATTAAAT	TATTAACCT	ATTATACTTAA	CAAAGTAGAGA	GGGAATCCAT	2640
TCTCTAGCTT	TCTGTGTTGG	TGCTTAATAT	TGGGGTAGGG	GGGGGGATCC	CCACAAATCA	2700
GGTCCCCTGA	GATAGCTGGT	CATTGGGGCT	ATCATGGCCA	GAATCTTCTT	CTCTGGGGT	2760
CTGGGGCCCC	AAAATGCTTA	ACCCAGGACC	TTGGAAAGTC	TACTCTATCC	AAATGATAAT	2820
TCCAAATGCT	GTTACCCAAG	GTAGGGGTG	TTGAAAGGAG	TAGAGGGTGG	GGCTTCAGGT	2880
CTCAACGGCT	TCTCCCTAACCA	CCCCCTCTCT	CTTGGGCCAG	CTGGTTTCCC	CCCACTTCCA	2940
CTCCCCCTTA	CTCTCTCTAG	GAATGGGCTG	ATGAAGGCAC	TGCCCCAAAT	TCCCCCTTACCC	3000
CCCAAACTTC	CCCTTACCCCC	AACTTTCCCC	ACCGACTCTCA	CAACCCCTTG	TGGGACTGACT	3060
GCAGGACGAG	AAGCACAAAG	TGCGGTTTCC	CAAGGGTTCTC	TCCATCTTCAG	CCCCCAGAGT	3120
ATATCTGTG	TGTTGGGAAATC	TCACACAGAA	ATCAGGAGC	ACCCCCCTGCC	TGAGCTTAAGG	3180
GAGGGCTTAT	CTCTTCAGGGG	GGGTAAAGT	GGCTTTGCA	ATATACTGTCG	CTTATTATTATT	3240
TAGCGGGGT	AAATTTTATAT	TAAGTCAGTGT	AGCAATCAGA	GTATAATGTG	TATGGTGACAA	3300
AAAAATTAAGG	CTTCTTATTA	TGTTTTAAAAA	AAAAAAAAAAA	AAAAAAAATAA	AAAAAAAAAAA	3360
AAAAAAAARA	AAAAAAAARA	AAAAAAAAAA	AAAAAAAAAA	AAAAAAAAAA	AAAAAAAAAA	3410

(2) INFORMATION FOR SEQ ID NO:111:

(i) SEQUENCE CHARACTERISTICS

- GENERAL CHARACTERISTICS:**

 - (A) LENGTH: 1289 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE-TYPE: CDNA

(vi) ORIGINAL SOURCE

- ORIGINAL SOURCE: U.S. GOVERNMENT

(xi) SEQUENCE DESCRIPTION: FIG. 1 shows the sequence of the first 100 amino acids of the protein.

AGCCAGGCT	CCCTCTGCT	GCCCCACTCAG	TGGCAACACC	CGGGAGCTGT	TTTGTCTT	6
GTGGAGCCCTC	AGCAGTTCCC	TCTTCAGAA	CTCACTGCCA	AGAGCCCTGA	ACAGAGGCCA	120
CCATGCAGTC	CTTCAGCTTC	ATTAGAACCCA	TGATGATCTT	CTTCATAATTG	CTCATCTTTC	180
TGTGTGGTGC	AGGCCCTGTG	CGAGTGGGCA	TCCTGGGTGTC	AATCGATGGG	GCATCTCTTC	240
TGAAGATCTT	CGGGGCACTG	TCTGCCAGTG	CCATGCACTG	TGTCAACCTG	GFGCTACTTCC	300
TCATCGCAGC	CGGGCTGTG	GTCTTGTGCTC	TTGGTTCCTC	GGGCTGCTAT	GGTGTCAAGA	360
CTGAGAGCAA	GTGTGGCTTC	TTGACGCTTC	TCTTCATCCT	CTCCCTCATC	TTCATGCTG	420
AGGTGGCAGC	TGCTGTGTTG	GCCTTGGTGT	ACACACCAAT	GGCTGAGGCC	TTCTCTGGCT	480
TGCTGTGTTG	QCCTGQCATC	AAGAAAAGAT	ATGGTFTCCCA	GGAAAGACTTC	ACTCAAGTGT	540
GGAACACCCAC	CATGAAAGGG	CTCAAGTGT	GGTGTCTTC	CAACATATAG	GATTGTTGAGG	600
ACTCACCTCA	CTTCAAAAGAG	AAACAGTGTCT	TTCCTCCATT	CTGTTGCAAT	GACAAACGTC	660
CCAAACAGCAG	TAATGAAAG	TGCAACAAAG	AAAAGGCTTC	CGACCCAGA	TTAGAGGGTT	720
GCTTCAATCA	GCTTTTGAT	GACATCGGAA	CTAATGCGAT	CACCGTGGGT	GGTGTGGCAG	780
CTGGAATTGG	GGGGCTCGAG	CTGGTGCGCA	TTGTTGTGTC	CATGTATCTG	TACTGCAATC	840
TAACAATAGT	CCACTTCTGC	CTCTGGCACT	ACTCTGCCTA	CTATGGGAACT	GTAAAGGAGC	900
ACCCCTGGCAA	GCAGCAGTGA	TTGGGGGAGG	GGACAGGACT	TAACATGCTC	ATCTGGGCCA	960
GAATGGACCT	GGCCCTTCTG	CTCCAGACTT	GGGGCTTAGAT	AGGGACCACT	CCTTTITAGCG	1020
ATGCTTGACT	TCTCTTCCAT	TGTTGGGTG	ATGGGTGGGG	GGCATTCTTCAG	AGCTCTTAAAG	1080
GTAGCCAGTT	CTGTTGCCCA	TTCCCCCAGT	CTTAAATACC	CTTGATATGC	CCCTCTAGGCC	1140
TAGTGTGAT	CCCGATGCTC	TACTGGGGGA	TGAGAGAAAG	GCATTTTATA	GCCTGGGCAT	1200
AACTGAAATC	AGCAGGACCT	CTGGGTGAT	GTGTAAGGG	CACTTCAAA	TGCTATAAAC	1260
TGTTACAATG	TTAAAAAAA	AAAAAAA				1288

(2) INFORMATION FOR SEQ ID NO:112:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 315 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:112:

Met Val Phe Thr Val Arg Leu Leu His Ile Phe Thr Val Asn Lys Gln
1 5 10 15

Leu Gly Pro Lys Ile Val Ile Val Ser Lys Met Met Lys Asp Val Phe
20 25 30

Phe Phe Leu Phe Phe Leu Gly Val Trp Leu Val Ala Tyr Gly Val Ala
35 40 45 50

Thr Glu Gly Leu Leu Arg Pro Arg Asp Ser Asp Phe Pro Ser Ile Leu
55 60

Arg Arg Val Phe Tyr Arg Pro Tyr Leu Gln Ile Phe Gly Gln Ile Pro
65 70 75 80

Gln Glu Asp Met Asp Val Ala Leu Met Glu His Ser Asn Cys Ser Ser
85 90 95

Glu Pro Gly Phe Trp Ala His Pro Pro Gly Ala Gln Ala Gly Thr Cys
100 105 110

Val Ser Gln Tyr Ala Asn Trp Leu Val Val Leu Leu Val Ile Phe
115 120 125

Leu Leu Val Ala Asn Ile Leu Leu Val Asn Leu Leu Ile Ala Met Phe
130 135 140

Ser Tyr Thr Phe Gly Lys Val Gln Gly Asn Ser Asp Leu Tyr Trp Lys
145 150 155 160

Ala Gln Arg Tyr Arg Leu Ile Arg Glu Phe His Ser Arg Pro Ala Leu
165 170 175

Ala Pro Pro Phe Ile Val Ile Ser His Leu Arg Leu Leu Arg Gln
180 185 190

Leu Cys Arg Arg Pro Arg Ser Pro Gln Pro Ser Ser Pro Ala Leu Glu
195 200 205

His Phe Arg Val Tyr Leu Ser Lys Glu Ala Glu Arg Lys Leu Leu Thr

210

215

220

Trp Glu Ser Val His Lys Glu Asn Phe Leu Leu Ala Arg Ala Arg Asp
 225 230 235 240

Lys Arg Glu Ser Asp Ser Glu Arg Leu Lys Arg Thr Ser Gln Lys Val
 245 250 255

Asp Leu Ala Leu Lys Gln Leu Gly His Ile Arg Glu Tyr Glu Gln Arg
 260 265 270

Leu Lys Val Leu Glu Arg Glu Val Gln Gln Cys Ser Arg Val Leu Gly
 275 280 285

Trp Val Ala Glu Ala Leu Ser Arg Ser Ala Leu Leu Pro Pro Gly Gly
 290 295 300

Pro Pro Pro Pro Asp Leu Pro Gly Ser Lys Asp
 305 310 315

(2) INFORMATION FOR SEQ ID NO:113:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 553 amino acids
- (B) TYPE: amino acid sequence
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE: Human

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:113:

Met Val Gln Arg Leu Trp Val Ser Arg Leu Leu Arg His Arg Lys Ala
 1 5 10 15

Gln Leu Leu Leu Val Asn Leu Leu Thr Phe Gly Leu Glu Val Cys Leu
 20 25 30

Ala Ala Gly Ile Thr Tyr Val Pro Pro Leu Leu Leu Glu Val Gly Val
 35 40 45

Glu Glu Lys Phe Met Thr Met Val Leu Gly Ile Gly Pro Val Leu Gly
 50 55 60

Leu Val Cys Val Pro Leu Leu Gly Ser Ala Ser Asp His Trp Arg Gly
 65 70 75 80

Arg Tyr Gly Arg Arg Arg Pro Phe Ile Trp Ala Leu Ser Leu Gly Ile
 85 90 95

Leu Leu Ser Leu Phe Leu Ile Pro Arg Ala Gly Trp Leu Ala Gly Leu
 100 105 110

Leu Cys Pro Asp Pro Arg Pro Leu Glu Leu Ala Leu Ile Leu Gly
115 120 125
Val Gly Leu Leu Asp Phe Cys Gly Gln Val Cys Phe Thr Pro Leu Glu
130 135 140
Ala Leu Leu Ser Asp Leu Phe Arg Asp Pro Asp His Cys Arg Gln Ala
145 150 155 160
Tyr Ser Val Tyr Ala Phe Met Ile Ser Leu Gly Gly Cys Leu Gly Tyr
165 170 175
Leu Leu Pro Ala Ile Asp Trp Asp Thr Ser Ala Leu Ala Pro Tyr Leu
180 185 190
Gly Thr Gln Glu Glu Cys Leu Phe Gly Leu Leu Thr Leu Ile Phe Leu
195 200 205
Thr Cys Val Ala Ala Thr Leu Leu Val Ala Glu Ala Ala Leu Gly
210 215 220
Pro Thr Glu Pro Ala Glu Gly Leu Ser Ala Pro Ser Leu Ser Pro His
225 230 235 240
Cys Cys Pro Cys Arg Ala Arg Leu Ala Phe Arg Asn Leu Gly Ala Leu
245 250 255
Leu Pro Arg Leu His Gln Leu Cys Cys Arg Met Pro Arg Thr Leu Arg
260 265 270
Arg Leu Phe Val Ala Glu Leu Cys Ser Trp Met Ala Leu Met Thr Phe
275 280 285
Thr Leu Phe Tyr Thr Asp Phe Val Gly Glu Gly Leu Tyr Gln Gly Val
290 295 300
Pro Arg Ala Glu Pro Gly Thr Glu Ala Arg Arg His Tyr Asp Glu Gly
305 310 315 320
Val Arg Met Gly Ser Leu Gly Leu Phe Leu Gln Cys Ala Ile Ser Leu
325 330 335
Val Phe Ser Leu Val Met Asp Arg Leu Val Gln Arg Phe Gly Thr Arg
340 345 350
Ala Val Tyr Leu Ala Ser Val Ala Ala Phe Pro Val Ala Ala Gly Ala
355 360 365
Thr Cys Leu Ser His Ser Val Ala Val Val Thr Ala Ser Ala Ala Leu
370 375 380
Thr Gly Phe Thr Phe Ser Ala Leu Gln Ile Leu Pro Tyr Thr Leu Ala
385 390 395 400

Ser Leu Tyr His Arg Glu Lys Gln Val Phe Leu Pro Lys Tyr Arg Gly
 405 410 415
 Asp Thr Gly Gly Ala Ser Ser Glu Asp Ser Leu Met Thr Ser Phe Leu
 420 425 430 435
 Pro Gly Pro Lys Pro Gly Ala Pro Phe Pro Asn Gly His Val Gly Ala
 435 440 445
 Gly Gly Ser Gly Leu Leu Pro Pro Pro Ala Leu Cys Gly Ala Ser
 450 455 460
 Ala Cys Asp Val Ser Val Arg Val Val Val Gly Glu Pro Thr Glu Ala
 465 470 475 480
 Arg Val Val Pro Gly Arg Gly Ile Cys Leu Asp Leu Ala Ile Leu Asp
 485 490 495
 Ser Ala Phe Leu Leu Ser Gln Val Ala Pro Ser Leu Phe Met Gly Ser
 500 505 510
 Ile Val Gln Leu Ser Gln Ser Val Thr Ala Tyr Met Val Ser Ala Ala
 515 520 525
 Gly Leu Gly Leu Val Ala Ile Tyr Phe Ala Thr Gln Val Val Phe Asp
 530 535 540
 Lys Ser Asp Leu Ala Lys Tyr Ser Ala
 545 550

(2) INFORMATION FOR SEQ ID NO:114:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 241 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:114:

Met Gln Cys Phe Ser Phe Ile Lys Thr Met Met Ile Leu Phe Asn Leu
 1 5 10 15
 Leu Ile Phe Leu Cys Gly Ala Ala Leu Leu Ala Val Gly Ile Trp Val
 20 25 30
 Ser Ile Asp Gly Ala Ser Phe Leu Lys Ile Phe Gly Pro Leu Ser Ser
 35 40 45
 Ser Ala Met Gln Phe Val Asn Val Gly Tyr Phe Leu Ile Ala Ala Gly

50 55 60
Val Val Val Phe Ala Leu Gly Phe Leu Gly Cys Tyr Gly Ala Lys Thr
65 70 75 80
Glu Ser Lys Cys Ala Leu Val Thr Phe Phe Ile Leu Leu Ile
85 90 95
Phe Ile Ala Glu Val Ala Ala Val Val Ala Leu Val Tyr Thr Thr
100 105 110
Met Ala Glu His Phe Leu Thr Leu Leu Val Val Pro Ala Ile Lys Lys
115 120 125
Asp Tyr Gly Ser Gln Glu Asp Phe Thr Gln Val Trp Asn Thr Thr Met
130 135 140
Lys Gly Leu Lys Cys Cys Gly Phe Thr Asn Tyr Thr Asp Phe Glu Asp
145 150 155 160
Ser Pro Tyr Phe Lys Glu Asn Ser Ala Phe Pro Pro Phe Cys Cys Asn
165 170 175
Asp Asn Val Thr Asn Thr Ala Asn Glu Thr Cys Thr Lys Gln Lys Ala
180 185 190
His Asp Gln Lys Val Glu Gly Cys Phe Asn Gln Leu Leu Tyr Asp Ile
195 200 205
Arg Thr Asn Ala Val Thr Val Gly Gly Val Ala Ala Gly Ile Gly Gly
210 215 220
Leu Glu Leu Ala Ala Met Ile Val Ser Met Tyr Leu Tyr Cys Asn Leu
225 230 235 240
Gln

(2) INFORMATION FOR SEQ ID NO:115:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 366 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo Sapiens

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:115:

GCTCTTCTC TCCCCCTCTC TGAATTAAAT TCTTTCAACT TGCAATTGC AAGGATTACA	60
CATTTCAGTG TGATGTATAT TGTTGGCAA AAAA..... GTGTCTTGT TTAAAATTAC	120
TTGGTTGTG AATCCATCTT GCTTTTCCC CATTGGAACT AGTCATTAAC CCACTCTGA	180
ACTGGTAGAA AAACATCTGA AGAGCTAGTC TATCAGCATC TGACAGGTGA ATTGGATGCT	240
TCTCAGAACC ATTTCACCCA GACAGCCTGT TTCTATCTG TTTAATAAAT TAGTTGGT	300
TCTCTACATG CATAACAAAC CCTGCTCCAA TCTGTCACAT AAAAGCTGTG GACTTGAAGT	360
TTAGTC	366

(2) INFORMATION FOR SEQ ID NO:116:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 282 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:116:

ACAAAGATGA ACCATTTCTC ATATTATAGC AAAATTAAAA TCTACCCGTA TTCTAATATT	60
GAGAAATGAG ATNAACACA ATNTTATAAA GTCTACTTGT AGAAAGATCAA GTGACCTCAA	120
AGACTTTACT ATTTTCACTAT TTAAAGACAC ATGATTTATC CTATTTAGT AACCTGGTTC	180
ATACGTTAA CAAAGGATAA TGTGAACAGC AGAGGAGATT TGTTGGCAGA AAATCTATGT	240
TCAATCTNGA ACTATCTANA TCACAGACAT TTCTATTCTT TT	282

(2) INFORMATION FOR SEQ ID NO:117:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 305 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:117:

ACACATGTGG CTTCACTGCC TTCTTAGAGTC CTCTCGGTCA ACATANAGGA ACAGGGACCA	60
TATTATCTT CCCTCTGAA ACAATTGCAA AATAANACAA AATATATGAA ACAATTGCAA	120
AATAAGGCAA AATATATGAA ACAACAGGTG TCGAGATATT GGAAATCAGT CAATGAAGGA	180
TACTGATCCC TGATCACTGT CCTAATGCGAG GATGTGGAA ACAGATGAGG TCACCTCTGT	240
GACTGCCCA GCTTACTGCC TGTAGAGAGT TTCTANGCTG CAGTTCAGAC AGGGAGAAAT	300
TGGGT	305

(2) INFORMATION FOR SEQ ID NO:118:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 71 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:118:

ACCAAGGTGT NTGAATCTCT GACGTGGGGA TCTCTGATT CCGCACAAATC TGAGTGGAAA	60
AANTCCCTGGG T	71

(2) INFORMATION FOR SEQ ID NO:119:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 212 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:119:

ACTCCGGTTG GTGTCAGCAG CACGTGGCAT TGAACATNGC AATGTGGAGC CCAAAACACA	60
GAAAATGGGG TGAATTTGGC CAACCTTCTA TNAACCTTAAG TTGGAANNT TGCCACCAAC	120
AGTAAGCTGG CCCTTCTAAAT AAAAGAAAAT TGAAAGGTGT CTCACTAANC GGAATTAAANT	180
ATGGANTCA AGANACTCCC AGGCCTCAGC GT	212

(2) INFORMATION FOR SEQ ID NO:120:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 90 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:120:

ACTCGTTGCA NATCAGGGC CCCCCAGAGT CACCGTTGCA GGAGTCCTTC TGGTCTTGCC	60
CTCCGCCGGC GCAGAACATG CTGGGGTGGT	90

(2) INFORMATION FOR SEQ ID NO:121:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 218 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:121:

TGTANCGTGA ANACGACAGA NAGGGTTGTC AAAATGGAG AACCTTGAA GTCATTGAA	60
GAATAAGATT TGCTAAAGA TTGGGGCTA AAACATGGTT ATTGGGAGAC ATTCCTGAAG	120
ATATNCANGT AAATTANGGA ATGAATTCACT GGTTCTTTG GGAATTCCCT TACGATNGCC	180
AGCATANACT TCATGTGGGG ATANCAGCTA CCCITGTAA	218

(2) INFORMATION FOR SEQ ID NO:122:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 171 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:122:

TAGGGGTGTA TGCAACTGTA AGGACAAAAA TTGAGACTCA ACTGGCTTAA CCAATAAACG	60
CATTITGTTAG CTCATGGAAC AGGAAGTCGG ATGGTGGGGC ATCTTCAGTG CTGCATGAGT	120
CACCACCCCG CGGGGGTCAT CTGTGCCACA GTTCCCTGTG GACAGTGCCTG T	171

(2) INFORMATION FOR SEQ ID NO:123:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 76 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:123:

TGTAGCGTGA AGACNACAGA ATGGTGTGTC CTGTGCTATC CAGGAACACA TTTATTATCA	60
TTATCAANTA TTGTGT	76

(2) INFORMATION FOR SEQ ID NO:124:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 131 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:124:

ACCTTTCCCC AAGGCCAATG TCCGTGTCG TAACTGGCCG GCTGCAGGAC AGCTGCAATT
 CAATGTCGTG GGTCAATATGG AGGGGAGGAG ACTCTAAAT AGCCAATT TT ATTCTCTTGG
 TTAAGATTG T

60
120
131

(2) INFORMATION FOR SEQ ID NO:125:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 432 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:125:

ACTTTATCTA CTGGCTATGA AATAGATGGT GGAAAATTGC GTTACCAACT ATACCACCTGG
 CTTGAAAAG AGGTGATAGC TCTTCAGAGG ACTTGTGACT TTTGCTCAGA TGCTGAAGAA 60
 CTACAGCTCG CATTGGCG AAATGAGAAT GAATTGGAT TAAATGAGGA TGCTGAAGAT 120
 TTGCGCTCAC AAACAAAATG GAACAAACTG AGAGAAAAATT TTCAGAAAAA AAGACAGTGG 180
 CTCTTGAACT ATCAGTCACT TTTGAGAATG TTCTTAGTT ACTGCATACT TCATGGATCC 240
 CATGGTGGGG GTCCTTCATC TGTAAGAATG GAATTTGTT TGCTTTGCA AGAACATTCAG 300
 CAGGAACAT CAGAACCACT ATTTCTAGC CCTCTGTCAG AGCAACCTTC AGTCCTCTC 360
 CTCTTGTCTT GT 420
 432

(2) INFORMATION FOR SEQ ID NO:126:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 112 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:126:

ACACAACTTG AATAGTAAAA TAGAACTGA GCTGAAATT CTAAATTCACT TTCTAACCAT
 AGTAAGAATG ATATTTCCCC CCAGGGATCA CCAAATATTATAAAAATT GT

60
112

(2) INFORMATION FOR SEQ ID NO:127:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 54 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:127:

ACCACGAAAC CACAAACAAG ATGGAAGCAT CAATCCACTT GCACAGCACAGCAG

54

(2) INFORMATION FOR SEQ ID NO:128:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 323 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:128:

ACCTCATTAG TAATTGTTTT GTTGTGTTCTAT TTTTTTCTAA TGTCTCCCCT CTACCAAGCTC
 ACCTGAGATA ACAGAAATGAA ATGGAAAGGA CAGCCAGATT TCTCTCTTCG TCTCTCTCTCA
 TTCTCTCTGA AGTCTAGGTT ACCCATTGTT GGGACCCATT ATTAGGAAATA AACACAGTT
 CCAAAGCAT TGGACAGTTT CTGTTGTTGT TTTAGAATGG TTTCTCTTT TCTTAGCCT
 TTCTGCCTAA AGGCTCACTC AGTCCCTTG CGTCTCAGTG GACTGGGCTC CCCAGGGCTC
 AGGCTGCCTT CTTTCCATG TCC

60
120
180
240
300
323

(2) INFORMATION FOR SEQ ID NO:129:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 192 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:129:

ACATACATGT GTGTATATTG TTAATATCA CTTTGTATC ACTCTGACTT TTTAGCATAC	60
TGAAAACACA CTAACATAAT TTNTGTGAAC CATGATCAGA TACAACCCAA ATCATTCACT	120
TAGCACATTC ATCTGTGATA NAAAGATAGG TGAGTTCTAT TTCCCTTCAGG TTGGCCAATG	180
GATAAACAAA GT	192

(2) INFORMATION FOR SEQ ID NO:130:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 362 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:130:

CCCTTTTTTA TGGATGAGT AGACTGTATG TTTGAANATT TANCCACAAAC CTCTTTGACA	60
TATAATGACG CAACAAAAAG GTGCTGTTTA GTCCCTATGGT TCAGTTTATG CCCCTGACAA	120
GTTCATTCATG TTGTTTGCGG ATCTCTCGGC TAATCGTGGT ATCTCTCCATG TTATTAGTAA	180
TTCTGATTTC CATTITGGTTA ACGCTCTGGT GATGTAACCT GCTANGAGGC TAACCTTATA	240
CTTATTTAAA AGCTCTTATT TTGTTGTCAT TAAATGGCA ATTATATGTGC AGCACTTTAT	300
TGCAGCAGGA AGCACCTGTG GGTTGGTTGT AAAGCTCTT GCTAATCTTA AAAAGTAATG	360
GG	362

(2) INFORMATION FOR SEQ ID NO:131:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 332 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:131:

CTTTTTGAAA GATCGTGTCC ACTCCTGTGG ACATCTTGTG TTAATGGAGT TTCCCATGCA	60
GTANGACTGG TATGGTTGCA GCTGTCCAGA TAAAAACATT TGAGAGGCTC CAAAATGAGA	120
GTTCTCCCG GTTGCCCTG CTGCTCCAG TCTCAGGAGC AGGCCCTTTT AGGAGGGCATC	180
TTCTGACTTA GATTAAGGCA GCTTGTAAAT CTGATGTGAT TTGGTTTATT ATCCAACTAA	240
CTTCATCTG TTATCAGCTG AGAAAGGCCA GACTCCCCAN GACNGGTAGC GATTGTGGC	300
ATANAAGGAT TGGGTGAAGC TGGCGTGTG GT	332

(2) INFORMATION FOR SEQ ID NO:132:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 322 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:132:

```

ACTTTTGCCA TTTTGATAT ATAAACAATC TTGGGACAIT CTCCCTGAAAAA CTAGGTTGCC      60
AGTGGCTAAG AGAACTCGAT TTCAAGCAAT TCTGAAGGG AAACCGAGCAT GACACAGAAAT     120
CTCAAATTC CAAACAGGGG CTCTGTGGGA AAAATGAGGG AGGACCTTTC TATCTCGGGT     180
TTAGCAAGT TAAAATGAAAT ATGACAGGAA AGGCTTATTTC ATCAACAAAG AGAACAGATTG    240
GGATGCTCT AAAAAAAGT TTGGTAGAGA AAATAGGAAT GCTNAATCCT AGGGAAGGCT     300
GTAACAATCT ACAATTGGTC CA                                         322

```

(2) INFORMATION FOR SEQ ID NO:133:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 278 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:133:

```

ACAAGCCTTC ACAAGTTAA CTAATTGGG ATTAATCTT CTGTANTTAT CTGCATAATT      60
CTTGTTTTTC TTTCATCTT GCTCCCTGGGT TGACAAATTG TGAAAACACAC TCTATTGCTA     120
CTATTTAAA AAAATCACAA ATCTTCCCTT TTAAGCTATG TTNTAATCCTT ACTTATTCCTG     180
CTATTCCTGT TTGTCAAAG AAATTTATT TTTCAAAAAA TGTTNTATTG TTGTGATGGGT     240
CCCACGAAAC ACTAATAAA ACCACAGAGA CCAGCCTG                                         278

```

(2) INFORMATION FOR SEQ ID NO:134:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 121 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:134:

GTAACTTAAACT TGTTTTCAA ATGTTATTT TACTTGATT TTGCTTTGG T	60 120 121
---	------------------

(2) INFORMATION FOR SEQ ID NO:135:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 350 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:135:

ACTTAAACCC ATGCCTAGCA CATCGAACCT CCTCAAAGAA CATCACTATA ATCCCTATAACC ATANCAAGTG GTGACTGGTT AAGCGTCGA CAAAGGTCAG CTGGCACATT ACTTGATGTGC AAACTTGATA CTTTTGTTTAA AGTAGGAGA TAGTATACAGA TNCCCTAGGAN TTGGTACTTCGA GGGTGCCCCC CAACCTCTGC AGCCGCTCTC CTGTGCCAGN CCCCCTGNAAGG AACCTTCGGT CCACCTCAAT CAACGCTCTG GCCATGCTAC CTGCAATTGG CTGAAACAAAC GTTTGCTGAG TTCCAAGGA TGCAAAGCCT GGTGCTCAAC TCCTGGGGCG TCAACTCAGT	60 120 180 240 300 350
---	---------------------------------------

(2) INFORMATION FOR SEQ ID NO:136:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 399 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:136:

TGTACCGTGA AGACGACAGA AGTTGCATGG CAGGGACAGG GCAGGGCCGA GGCCAGGGTT GCTGTGATGG TATCCGAATA NTCCCTCGTGA GAAAAGATAA TGAGATGAGC TGAGCAGGCT GCAGACTTGT GTCTGCCCTTC AANAAAGCCAG ACAGGAAGGC CCTGCCCTGCC TTGGCTCTGA CCTGGCGCC AGCCAGCCAG CCACAGGTGG GCTTCTTCTT TTGTTGGTGA CAACNCACAG AAAAGTCAG AGGCCCAAGG TCAGGTGTNA GTGGGTATG GACCATAAAAA CACCAAGGTGC TCCCAAGGAAC CGGGCAAAAG GCCATCCCCA CCTCACAGGCCA GCATGCCAC TGCGCTGATG GGTCAGAGN GATGAGGAGC CCAGNTGTTG TGCTGTGGT	60 120 180 240 300 360 399
--	--

(2) INFORMATION FOR SEQ ID NO:137:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 165 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:137:

ACTGGTGTGG TNGGGGTGA TGCTGGTGGT ANAAGTTGAN GTGACTTCAN GATGGTGTG	60
GGAGGAAGTG TGTTAACGTA GGGATGTAGA NGTTTGGCC GTGCTAAATG AGCTTCGGGA	120
TTGGCTGGTC CCACTGGTGG TCACTGTCAT TGGTGGGTT CCTGT	165

(2) INFORMATION FOR SEQ ID NO:138:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 338 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE: Homo sapiens

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:138:

ACTCACTGGA ATGCCACATT CACAACAGAA TCAGAGGCTCT GTGAAAACAT TAATGGCTCC	60
TTCACCTCTC CAGTAAGAT CAGGGGACTG AAATGGAAAC GTTAAACAGCC ACATGCCAA	120
TGCTGGCAG TCTCCCATGC CTTCACAGT GAAGGGCTT GAGAAAATC ACATCCAATG	180
TCATGTTT CCAGCACAC CAAAGGTCG TTGGGTGGA GGGCTGGGG CATANANGGT	240
CANGCTTCAG GAAGCTCAA GTTCCATTCA GCTTGGCCAC TGTACATTCC CCATNTTAA	300
AAAAACTGAT GCCTTTTTT TTTTTTTTG TAAAATTC	338

(2) INFORMATION FOR SEQ ID NO:139:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 382 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:139:

GGGAAATCTTG GTTTTTGGCA TCTGGTTTC CTATAGCCGA GGCCACTTTG ACAGAACAAA	60
GAAAGGGACT TCGAGTAAGA AGGTGATTAA CAGCCACGCT AGTGGCCGAA GTGAAGGAGA	120
ATTCAAAACAG ACCTCGTCAT TCCCTGGTGTG AGCCTGGTCG GCTCACCGCC TATCATCTGC	180

100

ATTTGCCCTTA CTCAGGTGCT ACCGGACTCT GGCCCCGTAT GTCTGTAGTT TCACAGGATG	240
CTTATTGCT CTTCTACACC CCACAGGGCC CCCTACTCTC TCGGATGTGT TTTTAATAAT	300
GTCAGCTATG TGCCCCATCC TCCCTCATGC CCTCCCTCCC TTTCCTACCA CTGCTGAGTG	360
GCCTGAACT TGTAAAGT GT	382

(2) INFORMATION FOR SEQ ID NO:140:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 200 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:140:

ACCAANCTT CTTCTGTG TGTTNGATTT TACTATAGGG GTTTNGCTTN TTCTAAANAT	60
ACTTTTCATT TAACANCTT TGTTAAGTGT CAGGCTGCAC TTGCTCCAT ANAATTATTG	120
TTCACAT TCAACTGTGA TGTTTGTC TCTTANAGCA TTGGTGAAT CACATATTG	180
ATATTCAAGCA TAAAGGAGAA	200

(2) INFORMATION FOR SEQ ID NO:141:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 335 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:141:

ACTTTATTTT CAAAACACTC ATATGTTGCA AAAAACAT AGAAAATAAA A3TTTGGTGG	60
GGGTGCTGAC TAAACCTAA GTCACAGACT TTTATGTC AGATGGAGC AGGGTTTGTGTT	120
ATGCATGTAG AGAACCCAAA CTAATTTATT AAACAGGATA GAAACAGGCT GTCTGGGTGA	180
AATGGTTCTG AGAACCATCC AATTCACTG TCAGATGCTG ATANACTAGC TCTTCAGATG	240
TTTTTCTACC AGTTCAAGAGA TNGGTTAATG ACTANTITCCA ATGGGGAAAA AGCAAGATGG	300
ATTCAACAC CAAGTAATT TAAACAAAGA CACTT	335

(2) INFORMATION FOR SEQ ID NO:142:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 459 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:142:

ACCAAGGTAA TATTGCCACA TATATCCCTT CCAATTGCGG GCTAAACAGA CGTGTATTAA	60
GGGTTGTTTA AAGACACACC AGCTTAAAT CAAGAGAAAT TTGTGACCTT CATGGAGTAT	120
CTGATGGAGA AAACACTGAG TTTCGACAAA TCTTATTTTA TTTCAGATAGC AGTCTGATCA	180
CACATGGTCC AACAAACACTC AAATAATAAA TCAAATATNA TCAGATGTTA AAGATTGGTC	240
TTCCAACATC ATAGCCCATC ATGGCCCGCT TGCCCTATAAT CTCTCCGACA TAAAACCACA	300
TCAACACCTC AGTGGCCACC AAACATTC GAACAGCTC CTTCAGCTTG AGCTGTTGAG	360
AGCTTACCACT CTGAGGCACTA TTGACTATNT TTTCANGCT CTGAATAGCT CTAGGGATCT	420
CAGCANGGTT GGGAGGAACC AGCTCAACCT TGGCGTANT	459

(2) INFORMATION FOR SEQ ID NO:143:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 140 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:143:

ACATTCCTT CCACCAAGTC AGGACTCTG GCTTCTGTGG GAGTTCTTAT CACCTGAGGG	60
AAATCCAAAC AGTCTCTCT AGAAAGGAAT AGTGTACACCA ACCCCACCCA TCTCCCTGAG	120
ACCATCCGAC TTCCCTGTGT	140

(2) INFORMATION FOR SEQ ID NO:144:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 164 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:144:

ACTTCAGTAA CAACATACAA TAACAACATT AAGTGTATAT TGCCATCTT GTCATTTCT	60
ATCTATACCA CTCTCCCTC TGAAAACAAN AATCACTANC CAATCACTTA TACAAATTG	120
AGGCAATTAA TCCATATTTG TTTTCAATAA GGAAAAAAAG ATGT	164

(2) INFORMATION FOR SEQ ID NO:145:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 303 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:145:

ACGTAGACCA TCCAACTTTG TATTGTAAT GGCAACATC CAGNAGCAAT TCCTAAACAA	60
ACTGGAGGGT ATTATACCC AATTATCCCA TTCAATTACA TGCCCTTC, CTCAAGGCTAT	120
GCAGGACAGC TATCATAAGT CGGCCAGGC ATCCAGATAC TACCATTTGT ATAAAACCTCA	180
GTAGGGGAGT CCATCCAAGT GACAGGTCTA ATCAAAGGG 60 GAAATGGAAC ATAAGCCCCAG	240
TAGTAAATTT TGCTTAGCT GAAACAGGCCA CAAAAGACTT ACCGCCGTGG TGATTACCAT	300
CAA	303

(2) INFORMATION FOR SEQ ID NO:146:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 327 base pairs;
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA.

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:146:

ACTGCAGGTC AATTAGAAGT GGTCTCTGAC TTTCATCANC TTCTCCCTGG GCTCCATGAC	60
ACTGGCCTGG AGTGAATCAT TGTCTCTGGTT GGTTGAGAGA GCTCCCTTGCG CAACAGGCT	120
CCAAGTCAGG GCTGGGATTG GTTTCCTTC CACATCTCTAG CAACAAATATG CTGGCCACTT	180
CCTGAAACAGG GAGGGTGGGA GGAGGCCAGCA TGGAAACAAAGC TGCCACTTTC TAAAGTAGCC	240
AGACTTGGCC CTGGGCTGT CACACCTACT GATGACCTTC TGTGCCATGCA GGATGGAATG	300
TAGGGGTGAG CTGTGTGACT CTATGGT	327

(2) INFORMATION FOR SEQ ID NO:147:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 173 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:147:

ACATTTGTTT TTTGAGATAA AGCATTGANA GAGCTCTCCCTAAACGTGACA CAATGGAGG	60
ACTGGAAAC ATACCCACAT CTTTGTTCG AGGGATAATT TTCTGATAAA GTCTTGCTGT	120
ATATTCAAGC ACATATGTTA TATATTATTC AGTTCCATGT TTATGCCCTA GTT	173

(2) INFORMATION FOR SEQ ID NO:148:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 477 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA (mRNA precursor)

(vi) ORIGINAL SOURCE: Human brain, frontal cortex, adult male

- (A) ORGANISM: *Homo sapiens*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:148:

ACAAACACTT TATCTCATCG AATTTTTAAC CCAAACACTAC TCACGTGCC TTTCTATCCT	60
ATGGGATATA TTATTGTATG CTCCATTTCA TCACACATTC ATGAAATAA CACTCATACT	120
GCCCTACTAC CTGCTGCAAT AACACATTC CCTTCCCTGTC CTGACCCCTGA AGCCATTGGG	180
GTGGTCTTAG TGCCCATCAG TCCANGCTG CACCTTGAGC CCTTGAGCTC CATTGTCAC	240
NCCANCCCCC CTACCGACCC CCATCTCTT ACACAGCTAC CTCCCTGCTC TCTAAACCCA	300
TAGATTATNT CCAAATTCAAG TCAATTAAAGT TACTTAAAC ACCTCTACCCG ACATGTCCAG	360
CCACACTGGT AAGGCCCTCTC CAGCCACAC ACACACACAC ACACNCACAC ACACACATAC	420
CCAGGCACAG GCTACCTCAT CTTCACAATC ACCCCCTTAA TTACCATGTC ATGGTGG	477

(2) INFORMATION FOR SEQ ID NO:149:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 207 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA (mRNA precursor)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Homo sapiens*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:149:

ACAGTTGTAT TATAATATCA AGAAATAAAC TTGCAATGAG AGCATTAAAG AGGGAAGAAC	60
TAACGTATT TAGAGAGCCA AGGAAGGTT CTGTGGGGAG TGGGATGTA GGTTGGGGCT	120
GATGATAAT AAGAGTCAGC CAGGTAAGT GGTTGGTGTGG TATGGGCACA GTGAAGAACAA	180
TTTCAGGAG AGGGAACAGC AGTGAAA	207

(2) INFORMATION FOR SEQ ID NO:150:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 111 base pairs

104

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:150:

ACCTTGATT CATTGCTGCT CTGATGGAAA CCCAACTATC TAATTTAGCT AAAACATGGG 60
 CACTTAAATG TGGTCAGTGT TTGGACTTGT TAACTANTGG CATCTTGGG T 111

(2) INFORMATION FOR SEQ ID NO:151:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 196 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:151:

AGCGCGGCAG GTCATATTGA ACATTCCAGA TACCTATCAT TACTCGATGC TGTTGATAAC 60
 AGCAAGATGG CTTTGAACCT AGGGTCAACCA CCAGCTATTG GACCTTACTA TGAAAACCAT 120
 GGATACCAAC CGGAAAACCC CTATCCCGCA CAGCCCACGT TGTCCCCCAC TGCTCTACGGAG 180
 GTGCATCCCG CTCAGT 196

(2) INFORMATION FOR SEQ ID NO:152:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 132 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:152:

ACAGCACTTT CACATGTAAAG AAGGGAGAAA TTCCTAAATG TAGGAGAAAAG ATAACAGAAC 60
 CTTCCCCCTTT TCATCTAGTG GTGGAAACCT GATGCTTAT GTTGACAGGA ATAGAACCAG 120
 GAGGGAGTTT GT 132

(2) INFORMATION FOR SEQ ID NO:153:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 285 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (vi) ORIGINAL SOURCE:
- (A) ORGANISM: *Homo sapiens*
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:153:
- ```

ACAAANACCA NGANAGGCCA CTGGCCGTG TGTCATGGCC TCCAAACATG AAAGTGTAG 60
CTTCTGCCTT TATGTCTCTA TCTGACAATCTTACCATTTATCCCTCG CTCAGCAGGA 120
GCACATCAAT AAAGTCAAA GCTCTGGACTTGCCCTTGCG TTGGAGGAAG TCATGACACAC 180
CCTGGCTAGT GAGGGTGGCG CGCCGCTCT GGATGACGGC ATCTGTGAAG TCGTCACCA 240
GTCTGCAGGC CCTGTGAAAG CGCCGTCAC ACGGAGTNAG GAATT 285

```
- (2) INFORMATION FOR SEQ ID NO:154:
- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 333 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (vi) ORIGINAL SOURCE:
- (A) ORGANISM: *Homo sapiens*
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:154:
- ```

ACACACAGTCC TGTGGGGCCA GGGCTTCATG ACCCTTTCTG TGAAAAGCCA TATTATCACC 60
ACCCCCAAATT TTTCCTTAAGA TATCTTTAAC TGAAGGGGTC AGCCTCTGA CTGCAAAGAC 120
CCTAAGCCGG TTACACAGCT AACTCCCCTACT GGCCTTGATT TGTTGAAATTG CTGCTGCCTG 180
ATTGGCACAG GAGTCGAAGG TGTTCAAGCTC CCCCTCTCCG TGGAACGAGA CTCTGTATTG 240
AGTTTCAACAA ATTCTCGGGC CACCTCGCA TTGCTCTCTG GAAATAAAA CGCGAGAAATG 300
GTCAGGCTG TCTCATCCAT ATGGATCTTC CGG 333

```
- (2) INFORMATION FOR SEQ ID NO:155:
- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 308 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (vi) ORIGINAL SOURCE:
- (A) ORGANISM: *Homo sapiens*
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:155:

ACTGGAAATA ATAAAACCCA CATCACAGTG TTGTGTCAA GATCATCAGG GCATGGATGG	60
GAAAGTGCCT TGGGAACGT AAAGTGCCTA ACACATGATC GATGATTTTT GTTATAATAT	120
TTGAATCAGC GTGCATACAA ACTCTCTGC CTGCTCTCC TGGGCCCCAG CCCCCAGCCC	180
ATCACAGCTC ACTGCTCTGT TCATCCAGGC CCAGCATGTA GTGGCTGATT CTTCTTGCT	240
GCTTITAGCC TCCANAAGTT TCTCTGAAGC CAACCAAACC TCTANGTGTAGGGATGCTG	300
GCCTCTGGT	308

- (2) INFORMATION FOR SEQ ID NO:156:
- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 295 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo sapiens
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:156:

ACCTTGCTCG GTGCTTGGAA CATATTAGGA ACTCAAAATA TGAGATGATA ACAGTGCCTA	60
TTATTGATTA CTGAGAGAAC TGTAGACAT TTAGTGAAG ATTTCCTACA CAGGAAGTGA	120
GAATAGGAGA TTATGTTGG CCCTCATATT CTCTCCATTC CTCCCTGCT CATTCTATGT	180
CTAATATATT CTCAATCAA TAAGGTAGC ATAATCAGGA AATGCCCAA ATACCAATAT	240
AAAACCAGAT GTCTATCCTT AAGATTTICA AATAGAAAAC AATTAACAG ACTAT	295

- (2) INFORMATION FOR SEQ ID NO:157:
- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 126 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo sapiens
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:157:

ACAAGTTAA ATAGTGCCT CACTGTGCAT GTGCTGAAAT GTGAAATCCA CCACATTCT	60
GAAGAGCAAA ACAAAATTCTG TCATGTAAATC TCTATCTGG GTCTGGGTA TATCTGTCCC	120
CTTAGT	126

- (2) INFORMATION FOR SEQ ID NO:158:
- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 442 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA
 (vi) ORIGINAL SOURCE: human liver
 (A) ORGANISM: *Homo sapiens*
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:158:

ACCCACTGGT	CTTGGAAACA	CCCATCCTTA	-ATACGATGAT	TITTCCTGTCC	TGTGAAAATG	60
ANCCAGCG	GCTGCCCTTA	GTCAGTCCTT	CCTTCCAGG	AAAAAGAGAT	TTGAGAAAGT	120
GCCTGGGATA	TTCACCAATT	ATTTCTCTCC	CCAAACTCTC	-TGAGTCCTCC	CTTAATATT	180
CTGGTGGTTC	TGACCAAAGC	AGGTGATGTT	TTGTGAGCA	TTTGGGATCC	-CAGTGAAGTA	240
NATTTGTTGA	GCCTTGCAATA	CTTAGCCCTT	CCACGCCAA	AACGGAGTGG	CAGAGTGGT	300
CCAACCCGT	TTTCCCCAGTC	CACGTAGACA	GATTACAGT	CGCGGATTCT	CGGAAGCTGG	360
NACAGACGGG	CTCTTTGAG	AGCCGGGACT	CTGAGANGGA	CATGAGGGCC	TCTGCTCTG	420
TGTTCATCTT	CTGATGTCCT	GT				442

(2) INFORMATION FOR SEQ ID NO:159:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 498 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: cDNA
 (vi) ORIGINAL SOURCE: human liver
 (A) ORGANISM: *Homo sapiens*
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:159:

ACTTCCAGGT	AACGTGTTG	TITCCGTTGA	GCCGTGAAGCT	ATGGGTGACG	TTGTAGGTTTC	60
TCCAAACAAGA	ACTGAGGTTG	CAGAGCGGGT	AGGGAAAGAT	GCTGTTCCAG	TTGCACCTGG	120
GCTGCTGTGG	AGCTGTTGTTG	ATTCCTCACT	ACGGCCCAAG	TTGTGGAAC	TGGCANAAAG	180
GTGTTGTTG	AGGANTGAGC	TCCGGCGGT	GTGTTAGGT	GTGGGCTCTT	CAACAGGGGC	240
TGCTGTTGTC	CCGGGANGTG	AANGTGTGTTG	GTCACTTGAG	CTTGGCCAGC	TCTGGAAAGT	300
ANTANATCT	TCTCTGAGGC	CAGCGCTTGT	GGAGCTGGCA	NGGGCTANTC	TTGTGTGTA	360
CGAACCGATG	CTGCTGTGGG	TGGGTGTANA	TCTCTCCAAAA	AGGCTGAAGT	TATGGTGTCTN	420
TCAGGTAANA	ATGTGGTTTC	AGTGTCCCTG	GGCNGCTGTG	GAAGGTGTGA	NATTGTCAAC	480
AAGGAAATAA	GCTGTTGGT					498

(2) INFORMATION FOR SEQ ID NO:160:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 380 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: cDNA
 (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Homo sapiens*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:160:

ACCTGCATCC	AGCTTCCCAG	CCAAACTCAC	AAGGAGACAT	CAACCTCTAG	ACAGGGAAC	60
AGCTTCAGGA	TACTTCCAGG	AGACAGAGCC	ACCAGCAGCA	AAACAAATAT	TCCCCATGCC	120
GGAGCATGCG	ATAGAGGAAG	CTGAAAATG	TGGGGTGTGA	GGAAAGCCATT	TGAGTCTGGC	180
CACTAGACAT	CTCATCAGCC	ACTTGTGTGA	AGAGATGCC	CATGACCCCA	GATGCCCTTC	240
CCACCTTAC	CTCCATCTCA	CACACTTGAG	CTTCCCCTC	TGTATAATTC	TAACATCTCG	300
GAGAAAAATG	GCAGTTTGAC	CGAACCTGTT	CACACCGTA	GAGGCTGATT	TCTAACGAAA	360
CTTGTAGAAT	GAAGCCTGGA					380

(2) INFORMATION FOR SEQ ID NO:161:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 114 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:161:

ACTCCACATC	CCCTCTGAGC	AGGGGGTTGT	CGTTCAAGGT	GTATTTGGCC	TTGCCCTGTCA	60
CACTGTCCAC	TGGCCCTTA	TCCACTGTG	GCTTAATCCC	TCGAAAGAGC	ATGT	114

(2) INFORMATION FOR SEQ ID NO:162:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 177 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:162:

ACTTTCTGAA	TCGAATCAA	TGACTACTTAG	TGTAGTTTA	ATATCCTCAT	ATATATCAA	60
GTTTTACTAC	TCTGATAATT	TGTAAACCA	GGTAACCCAGA	ACATCCAGTC	ATACAGCTT	120
TGGTGATA	TAACTTGGCA	ATAACCCAGT	CTGGTGATAC	ATAAAACTAC	TCACTGT	177

(2) INFORMATION FOR SEQ ID NO:163:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 137 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:163:

CATTATACCA GACAGGCGTG AAGACATCA CGACAAAAAC GCGAAATTCT ATCCCGTGCAC	60
CANAGAAGGC AGCTACGGCT ACTCTACAT CCTGGCGTGG GTGGCCTTCG CCTGCACCTT	120
CATCAGGGC ATGATGT	137

(2) INFORMATION FOR SEQ ID NO:164:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 469 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:164:

CTTATCACAA TGAATGTTCT CCTGGGCAGC GTTGTGACTT TTGCCACCTT CGTGACTTTA	60
TGCAATGCA CATGCTATT CATACTTAA GAGGGACTTC CAGGAGATTC AACAGGAAA	120
TGCGATGTC CTTGCTACGA AACAGAAAATTC TCATGTTGCA CCCCTGTTC TACACCTGTG	180
GAGACATGCA GGTTATGACA AACAGAAACTG CCAAAGAACATC TTCAAGAAGG AGGACTGCAA GTATATCGTG	240
GTGAGAGAAGA AGGAGGAAACAA AAAGACCTGT TCTGTGAGTG AATGGATAAT CTAATGTTGCT	300
TCTAGTAGGC ACAGGGCTTC CAGGCCAGGC CTCAATTCTCC TCTGGCCTT AATAGTCAT	360
GATTGTGAG CCATGCTTAT CAGTAAAAAG ATNTTTGAGC AACACCTTT	420
	469

(2) INFORMATION FOR SEQ ID NO:165:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 195 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:165:

ACAGTTTTT ATANATATCG ACATTGCGG CACTTGTGT CAGTTTCATA AAGCTGGTGG	60
ATCCGCTGTC ATCCACTATT CCTTGGCTAG AGTAAAAATT ATTCTTATAG CCCATGTCCC	120
TGCAGGCGC CGCGCCCTAG TTCTCGTTC AGTCGTCTTG GCACACAGGG TGCCAGGACT	180
TCCCTGAGA TGAGT	195

(2) INFORMATION FOR SEQ ID NO:166:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 383 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:166:

ACATCTTAGT AGTGTGGCAC ATCAGGGGC CATCAGGGTC ACAGTCACTC ATAGCCTCGC	60
CGAGGTCGGA GTCCACACCA CCGGTGTAAG TGTGCTCAAT CTTGGGCTTG GCGGCCACCT	120
TTGGAGAAAG GATATGCTGC ACACACATG CCACAAAGCC TGTGAACCTG CCAAAGAAATT	180
TITTCAGACCC AGCCTGAGCA AGGGCGGAT GTTCAGCTTC AGCTCCTCTC TCGTCAGGTG	240
GATGCCAACCC TCGTCTANGG TCCGTGGGAA GCTGGTGTCC ACNTCACCTA CAACCTGGGC	300
GANGATCTTA TAAAGAGGCT CCNAGATAAA CTCCACGAA CCTCTCTGGG AGCTGCTIAGT	360
NGGGGCTTT TTGGTGAACT TTC	383

(2) INFORMATION FOR SEQ ID NO:167:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 247 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:167:

ACAGAGCCAG ACCTTGGCCA TAAATGAANC AGAGATTAAG ACTAAACCCC AAGTCGANAT	60
TGGAGCAGAA ACTGGAGCAA GAAGTGGGCC TGGGGCTGAA GTAGAGACCA AGGCCACTGC	120
TATANCCATA CACAGAGCCA ACTCTCAGGC CAAGGCNATG GTTGGGCAG ANCCAGAGAC	180
TCAATCTGAG TCCAAAGTGG TGGCTGGAAC ACTGGTCATG ACANAGGCAG TGACTCTGAC	240
TGANGTC	247

(2) INFORMATION FOR SEQ ID NO:168:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 273 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:168:

ACTTCTAACT TTTCTAGAAC	TGGAAGGATT GTANTCATCC	TGAAAATGGG TTTACTTCAA	60
AATCCCTCAN CCTTGTTCTT	CACNACTGTC TATACTGANAG	TGTTCATGTT TCCACAAAGG	120
GCTGACACCT GAGCCCTGNA	TTCCTACTAT CCCTGAGAAC	CCCTTCCAG TAGGGTGGGC	180
AATTCCCAAC TTCCCTGCCA	CAAGCTCCC AGGCTTCTC	CCCTGGAAAA CTCCAGCTTG	240
AGTCCCGAT ACACTCATGG	GCTGCCCTGG GCA		273

(2) INFORMATION FOR SEQ ID NO:169:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 431 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (vi) ORIGINAL SOURCE:
- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:169:

ACAGCCTTGG CTTCCCCAAA	CTCCACAGTC TCAGTGCAGA	AAGATCATCT TCCAGCAGTC	60
AGTCAGACC AGGGTCAAAG	GATGTGACAT CAACAGTTTC	TGTTTCTAGA ACAGGTTCTA	120
CTACTGTCAA ATGACCCCCC	ATACTTCTC AAAGGCTGTG	GTAAGTTTTG CACAGGTGAG	180
GGCACGAGA AGGGGGTANT	TACTGTGAGA CACCATCTTC	TCTGTACTAC CCACACTGAC	240
CTTGCCATGG GCAAAAGGCC	CTTACACAAA AACAAATAGG	TCACTGTGG GCACCAAGCTC	300
ACGCACATCA CTGACAACCG	GGATGGAAAAA AGAANTGCCA	ACTTTCATAC ATCCAACCTGG	360
AAAGTGTCT GATACTGGAT	TCTTAATTAC CTTCAAAAGC	TTCTGGGGGC CATCAGCTGC	420
TCGAACACTG A			431

(2) INFORMATION FOR SEQ ID NO:170:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 266 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:170:

ACCTGTGGGC TGGGCTGTAA	TGCTGTGCC GGCTGCTGAA	AGGGAGTTCA GAGGTGGAGC	60
TCAAGGAGCT CTGCAAGCAT	TTTGCCAAAC CTCTCCANAG	CANAGGGAC AACCTTACACT	120
CCCCGCTAGA AAGACACCAAG	ATTGGAGTC TGCGGAGGGGG	AGTTGGGGTG GGCATTGAT	180
GTATACTGT CACCTGAAATG	AANGAGCCAG AGAGGAANGA	GACGAANATG ANATTGGCT	240
TCAAAGCTAG GGGTCTGGCA	GGTGGA		266

(2) INFORMATION FOR SEQ ID NO:171:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1248 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:171:

GGCAGCCCCAA	TCATAAACCGG	CGAGGACTGC	AGCCCGCACT	CGCAGCCCTG	GCAGGGGGCA	60
CTGGTCATGG	AAAACGATT	GTTCTGCTCG	GCGGTCTCTG	TGCATCCGCA	GTGGGTGCTG	120
TCAGCCGAC	ACTGTTTCA	GAAGTGTAGTG	CAGAGCTCT	ACACCATCGG	GCTGGGCCCTG	180
CACAGTCTTG	AGGGCGACCA	AGAGCCAGGG	AGCCAGATGG	TGGAGGCCAG	CCTCTCCGTA	240
CGGCACCCAG	AGTAAACACAG	ACCCCTTGCTC	GCTAACCGAC	TCATGCTCAT	CAAGTTGGAC	300
GAATCCGTTG	CCGAGTCTGA	CACCATCCGG	AGCATCAGCA	TTGCTTCGCA	GTGCCCCCTACC	360
CGGGGGAACT	CTTGGCTCTGT	TTCTGGCTGG	GGTCTGCTGG	CGAACCGCAG	AAATGCCCTACC	420
GTGCTGCACT	GGCTGAACGT	CGCTGGTGG	TCTTGAGGAGG	TCTGCACTAA	GCTCTATGAC	480
CCGGCTGTAC	ACCCACGAT	GTTCCTGGCC	GGCGGGAGGG	AAAGCAGGAA	GGACTCTTGC	540
AAACGGTACT	CTGGGGGGCC	CCTGATCTGC	AACGGTACT	TGCAAGGCCCCT	TGTTGCTCTTC	600
GGAAAAACCC	CGTGTGCGCA	AGTGGCCG	CGAGGTCTCT	ACACAAACCT	CTGCAAATTC	660
ACTGAGTGA	TAGAGAAAAC	CGTCCAGGGC	AGTTAACCTT	GGGGACTTGGG	AACCCATGAA	720
ATTGACCCCC	AAATACATCC	TGCGGAAGGA	ATTCAAGGAAT	ATCTGTTCCC	AGCCCCCTCT	780
CCCTCAAGCC	CAGGAGTCGA	GGCCCCCAGC	CTCCCTCCCTC	TCAAAACAAAG	GGTACAGATC	840
CCCAGCCCC	CCTCTTCAG	ACCCAGGAGT	CCAGACCCCC	CAGGCCCCCTC	TCCCTCAGAC	900
CCAGGAGTCC	AGCCCCCTCT	CCCTCAGACC	CAGGAGTCCA	GACCCCCCAG	CCCCCTCCCTC	960
CTCAGACCA	GGGGTCCAGG	CCCCCAACCC	CTCTCTCTC	AGACTCAAG	GTCCAAGGCC	1020
CCAACCCNT	ATTCGGGAG	CAGAGGGTC	CAGGTCCTCAG	CCCCCTCNCC	CTCAGACCCA	1080
GCGGTTCAAT	GCCACCTAGA	CTNTCCCTGT	ACACAGTGC	CCCTTGTGGC	ACGTTGACCC	1140
AACCTTACCA	GTGGTTTTT	CATTTTTNGT	CCCTTTCCCC	TAGATCAGA	AATAAAGTTT	1200
AAGAGAAGNG	AAAAAAAAAA	AAAAAAAAAA	AAAAAAAAAA	AAAAAAA	AAAAAAA	1248

(2) INFORMATION FOR SEQ ID NO:172:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 159 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:172:

Met Val Glu Ala Ser Leu Ser Val Arg His Pro Glu Tyr Asn Arg Pro

1 5 10 15

Leu Leu Ala Asn Asp Leu Met Leu Ile Lys Leu Asp Glu Ser Val Ser
 20 25 30
 Glu Ser Asp Thr Ile Arg Ser Ile Ser Ile Ala Ser Glu Cys Pro Thr
 35 40 45
 Ala Gly Asn Ser Cys Leu Val Ser Gly Trp Gly Leu Leu Ala Asn Gly
 50 55 60
 Arg Met Pro Thr Val Leu Gln Cys Val Asn Val Ser Val Val Ser Glu
 65 70 75 80
 Glu Val Cys Ser Lys Leu Tyr Asp Pro Leu Tyr His Pro Ser Met Phe
 85 90 95
 Cys Ala Gly Gly Gln Xaa Gln Xaa Asp Ser Cys Asn Gly Asp Ser
 100 105 110
 Gly Gly Pro Leu Ile Cys Asn Gly Tyr Leu Gln Gly Leu Val Ser Phe
 115 120 125
 Gly Lys Ala Pro Cys Gly Gln Val Gly Val Pro Gly Val Tyr Thr Asn
 130 135 140
 Leu Cys Lys Phe Thr Glu Trp Ile Glu Lys Thr Val Gln Ala Ser
 145 150 155

(2) INFORMATION FOR SEQ ID NO:173:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1265 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:173:

GGCAGCCCGC ACTCGCAGCC CTGGCAGGCC GCACGGTCA TGGAAAACGA ATTGTTCTGC	60
TGGGGCGTC TGGTGATCC GCAGTGGGTG CTGTCAGGCC CACACTGTTT CCAGAACCTCC	120
TACACCATCG GGCTGGGCCT GCACAGTCTT GAGGCCGACC AAAGGCCAGG GAGCCAGATG	180
GTGGAGGCCA GCCTCTCCGT ACGGCACCCA GAGTACAACA GACCCCTTGC CGCTAACGAC	240
CTCATGCTCA TCAAGTGGG CAAATCCGTG TCCGGACTCTG ACACATCCG GAGCATTGAGC	300
ATTGCTTCG AGTGGCCTAC CGGGGGGAAC CCTTGTCTCG TTTCGGCTG GGGTCTGCTG	360
GCGAACCGTG AGCTCACGGG TGTTGTTCTG CCCTCTCAA GGAGGTCCTC TCCCCAGTCG	420
CGGGGGCTGA CCCAGAGCTC TGCGTCAGGC CGACAAATGCC TACCGTCTG CAGTGGCTGA	480
ACGTGTCGGT GGTGTCCTGAG GAGGTCTGCA GTAAGCTCTA TGACCCGCTG TACCAACCCC	540
GCATGTTCTG CGCCGGCGGA GGGCAAGACC AGAAGGACTC CTGCAACGGT GACTCTGGGG	600
GGCCCCCTGAT CTGCAACGGG TACTTGCAGG GCCTTGTGTC TTTCGGAAAA GCCCCGTGTG	660
GCCAAGTTGG CGTGCCAGGT GTCTACACCA ACCCTCTGCAA ATTCACTGAG TGGATAGAGA	720

AAACCGTCCA	GGCCAGTTAA	CTCTGGGAC	TGGGAACCCA	TGAAATTGAC	CCCCAAATAC	780
ATCTGCGGA	AGGAATTAG	GAATATCTGT	TCCCAGCCC	TCCTCCCTCA	GGCCCAGGAG	840
TCCAGGCC	CAGCCCCCTCC	TCCCCTCAAAC	CAAGGGTACA	GATCCCCAGC	CCCTCTCTCC	900
TCAGACCC	GAGTCCAGAC	CCCCCAGCCC	TCCTCCCTC	AGACCCCAGA	GTCCAGCCCC	960
TCCTCCNTCA	GACCCAGAG	TCCAGACCCC	CCAGCCCCCTC	CTCCCTCAGA	CCCAAGGGTT	1020
GAGGCCCCCA	ACCCCTCTTC	CTTCAGAGTC	AGAGGTCCAA	GCCCCCAACC	CCTCGTTCCC	1080
CAGACCCAGA	GGTNNAGGTC	CCAGCCCCCTC	TTCCNTCAGA	CCCAAGNGTC	CAATGCCACC	1140
TAGATTTC	CTGNACACAG	TGCCCCCTTG	TGGNANGTTG	ACCCAACCTT	ACCAAGTTGGT	1200
TTTCATTTT	TNGTCCCTTT	CCCCTAGATC	CAGAAATAAA	GTTTAAGAGA	NGNGCAAAAA	1260
AAAAA						1265

(2) INFORMATION FOR SEQ ID NO:174:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1459 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:174:

GGTCAGCGGC	ACACTGTTTC	CAGAAAGTGA	TGCAAGCTC	CTACACCATC	GGGCTGGGCC	60
TGAGCGACT	TGAGGCCGAC	CAAGGCCAG	GGAGCCAGAT	GGTGGAGGGC	AGCCTCTCCG	120
TACCGCACCC	AGAGTACAAAC	AGACCCCTTC	TCGCTAACGA	CCTCATGCTC	ATCAAGTTGG	180
ACGAATCGGT	GTCCGAGTCT	GACACATCC	GGAGCATCAG	CATTGCTTCG	CAGTGCCTTA	240
CCGGGGGAA	TCTTGTGCTC	GTTCCTGCTG	GGGGTCTGCT	GGGGAAACGGT	GAGCTCACGG	300
GTGTGTGCT	GGCTCTTCA	AGGAGGTCT	CTGCCCCAGTC	GGCGGGGCTG	ACCCAGAGCT	360
CTGGGTCTCA	GGCAGAGTGC	CTACGGCTCT	GCAGTGTGG	AACGTGTGG	TGGTGTCTGA	420
NGAGGTCTG	NTAAAGCTCT	ATGACCCCT	GTACACCCC	ANCATGTTCT	GGCCGGCGGG	480
AGGGCAAGAC	CAGAGGACT	CCTGCAACGT	GAGAGAGGGG	AAAGGGGAGG	GCAGGGCACT	540
CAGGGAGAGG	TGGAGAAGGG	GGAGGAGAG	ACACACAGGG	CCGCATGGCG	AGATGCAAG	600
ATGGAGAGAC	ACACAGGGAC	ACAGTGACAA	CTAGAGAGAG	AAACTGAGAG	AAACAGAGAA	660
ATAAACACAG	GAATAAAAGAG	AAGCAAAGGA	AGAGAGAAAC	AGAACACAGAC	ATGGGGAGGC	720
AGAAAACACAC	ACACATAGAA	ATGCACTGAA	CTCTCCAAACA	GCATGGGGCC	TGAGGGCGGT	780
GACCTCCCA	CAATAGAAA	TCTCTTATA	ACTTTTGACT	CCCCAAAAC	CTGACTAGAA	840
ATAGCTCT	GTGACGGGG	AGCCTTACCA	ATAACATAAA	TAGTCGATT	ATGCATACGT	900
TTTATGCAAT	CATGATATAC	CTTTGTTGGA	ATTTTTGAT	ATTTCTAAGC	TACACAGTC	960
GTCTGTGAAT	TTTTTAAAT	TGTTGCACT	CTCCCTAAAT	TTTCTGTATG	TGTTTATTGA	1020
AAAAATCCAA	GTATAAGTGG	ACTTGTGAT	TCAAACCAGG	GTGTTCAAG	GGTCAACTGT	1080
GTACCCAGAG	GGAAAACAGTG	ACACAGATTC	ATAGAGGTGA	AAACAGAAGA	GAACAGAGAA	1140
AAATCAAGAC	TCTACAAAGA	GGCTGGCGAG	GGTGGCTCAT	GGCTGTTAATC	CCAGCACTTT	1200
GGGAGGGCGAG	GCAGGGAGAT	CACTTGAGGT	AAGGAGTCTA	AGACCCAGCT	GGCCAAAATG	1260
GTGAAATCCT	GTCTGTACTA	AAAATACAAA	AGTTAGCTGG	ATATGGTGGC	AGGCGGCTGT	1320
AATCCAGCT	ACTTGGGAGG	CTGAGGCAGG	AGAATGCTC	GAATATGGGA	GGCACAGGTT	1380
GAAGTGAAGT	GAGATCACAC	CACTATACTC	CAGCTGGGCC	AACAGAGTAA	GACTCTGTCT	1440
AAAAAAAAAA	AAAAAAAAAA					1459

(2) INFORMATION FOR SEQ ID NO:175:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1167 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE: human
(A) ORGANISM: *Homo sapiens*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:175:

GCGCACGCCCT	GGCAGGCGGC	ACTGGTCATG	GAAAACGAAT	TGTTCTGCTC	GGGCGTCCTG	60
GTGATCATGCCG	AGTGGCTGTG	GTCAAGCCCCA	CACTGTTTCG	AGAAACTCCTA	CACCATCGGG	120
CTGGGGCTGC	ACAGCTTGAG	GGCCGACCAA	GAGCCAGGGG	GGCCAGATGGT	GGAGGGCCACG	180
CTCTCCGTAC	GGCACCCAGA	GTACAAGACA	CTCTGGCTCG	CTAACGACCT	CATGCTCATC	240
AAGTGTGAGC	AATCCGTGTC	CGAGTCTGAC	ACCATCCCGA	GCATCAGCAT	TGCTTCGAG	300
TGGCTTACCG	CGGGGAACCT	TTGGCTCGTN	TCTGGCTGGG	GTCTGCTGCG	GAACGGCAGA	360
ATGCTTACCG	TGCTGCTAGT	CGTGAACATG	TCGGTGGTGT	TCGAGGANTG	TCGCTAGAAG	420
CTCTATGACC	CGCTGTGACCA	CCCCAGCATG	TTCTGCGCCG	GCGGAGGGCA	AGACCCAGAA	480
GACTCTGCA	ACGGTGTGACTC	TGGGGGGGCC	CTGATCTGCA	ACGGGTTACTT	GCAGGGCCCT	540
GTGCTTCTTC	GGAAAGCCCC	GTGTTGGCAA	TTCTGGCTGC	CAGGTGCTTA	CACCAACCTC	600
TGCAAATTC	CTGAGTGGAT	AGAGAAAACC	GTCCAGNCCA	GTAACTCTG	GGGAATGGGA	660
ACCCATTGAA	TTGAGCCCCA	AATACATCTC	GGCGGAANGAA	TTCAAGGAATA	TCTGTTCCCA	720
GCCCCCTCTC	CTTCAGGGCCC	AGGAGTCAG	GGCCCCCGGCC	CCTCTCTCCCT	CAAACCAAGG	780
GTACAGATCC	CCAGCCCCCTC	CTCCCTCAGA	CCCAGGAGTC	CAGACCCCCC	AGCCCCCTNT	840
CCNTCAGACC	CAAGGGATCCTA	GGCCCCCTCTC	CNTCAGACGC	AGGAGTCCAG	ACCCCCCAGC	900
CCNTCAGTCG	TCAGACCCAG	GGGTGAGGCC	CCCCAACCCC	TCTNCNTCTA	GAGTCAGAGG	960
TCCAAGCCCC	CAACCCCTCG	TTCCCCAGAC	CGAGAGTNC	AGGTCCTCAG	CCCTCCCTCC	1020
TCAGACCCAG	CGGTCTTCAATG	CCACCTAGAN	TNTCTCTGTG	CACAGTGCCC	CCTTGTGGCA	1080
NTGTTGACCA	ACCTTACCG	TTGGTTTTTC	ATTTTTTGTC	CTTTTCCCTC	AGATCCAGAA	1140
ATAAAAGTNTA	AGAGAACGCC	AAAAAAA				1167

(2) INFORMATION FOR SEQ ID NO:2764

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 205 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:376

Val Leu Ser Ala Ala His Cys Phe Gln Asn Ser Tyr Thr Ile Gly Leu
20 25 30

Gly Leu His Ser Leu Glu Ala Asp Gln Glu Pro Glu Ser Glu Val

35	40	45
Glu Ala Ser Leu Ser Val Arg His Pro-Glu Tyr Asn Arg Leu Leu Leu		
50	55	60
Ala Asn Asp Leu Met Leu Ile Lys Leu Asp Glu Ser Val Ser Glu Ser		
65	70	75
Asp Thr Ile Arg Ser Ile Ser Ile Ala Ser Gln Cys Pro Thr Ala Gly		
85	90	95
Asn Ser Cys Leu Val Ser Gly Trp Gly Leu Leu Ala Asn Gly Arg Met		
100	105	110
Pro Thr Val Leu His Cys Val Asn Val Ser Val Val Ser Glu Xaa Val		
115	120	125
Cys Ser Lys Leu Tyr Asp Pro Leu Tyr His Pro Ser Met Phe Cys Ala		
130	135	140
Gly Gly Gly Gln Asp Gln Lys Asp Ser Cys Asn-Gly Asp Ser Gly		
145	150	155
Pro Leu Ile Cys Asn Gly Tyr Leu Gln Gly-Leu Val Ser-Phe Gly Lys		
165	170	175
Ala Pro Cys Gly Gln Leu Gly Val Pro Gly Val Tyr Thr Asn Leu Cys		
180	185	190
Lys Phe Thr Glu Trp Ile Glu Lys Thr Val Glu Xaa Ser		
195	200	205

(2) INFORMATION FOR SEQ ID NO:177:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1119 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo sapiens

GCGCACTCGC	AGCCCCGCGA	GGCGGCACTG	GTCATGGAAA	ACGAATTGTT	CTGCTCGGGC	60
GTCCTGGTGC	ATCCGCACTG	GGTGTCTGTC	GCCGCAACT	TTTTCCAGAA	CTCCCTACACC	120
ATCCGGCTGC	GGCTCGACAG	TCTTGAGGCC	GACCAAGAGC	CAGGGAGGCC	GATGGTGGAG	180
GCCAGCTCT	CTCGTACGGCA	CCCAGAGTC	AACAGACCTT	TGCTCTCTAA	CGACCTCATG	240
CTCATCAAGT	TGGACGAATC	CGTGTCCGAG	TCTGACACCA	TCCGGAGCAT	CAGCATTGCT	300
TCGCACTGCC	CTACCGCGGG	GAACCTCTGC	CTCTGTTCTG	GCTGGGGTCT	GCTGGCGAAC	360
GATGCTGTGA	TTGCCCATCA	GTCCCGAGCT	GTGGGGGGCT	GGGAGTGTGA	GAAGCTTTCC	420
CAACCTCTGGC	AGGGTGTAC	CATTCTGGCA	ATCTTCCAGTG	CAAGAGCTC	CTGCTCGCATC	480

CTCACTGGGT	GCTCACTACT	GCTCACTGCA	TCACCCGAA	CACTGTGATC	AACTAGCAG	540
CACCATAGTT	CTCCGAAGTC	AGACTATCAT	GATTACTGTG	TTGACTGTGC	TGTCTATTGT	600
ACTAACCATG	CCGATGTTTA	GOTGAATTA	GCGTCACTTG	GCTCAACCA	TCTTGGTATC	660
CAGTTATCCT	CACTGAATTG	AGATTCTCTG	CTTCAAGGAT	GCTGGTACTC	CCCTCACAAA	720
TGACCTACAG	AGGTGAGGGG	TCATATAGCT	CTTCAAGGAT	GCTGGTACTC	CCCTCACAAA	780
TTCATTTCTC	CTGTTGTA	GAAAGGTGCG	CCATTCTGGAG	CTCCCCAGGG	TGGGTGTGCA	840
GGTCACAATG	ATGAATGTA	GATCGTGTTC	CCATTACCCA	AAGCCTTAA	ATCCCTCATG	900
CTCAGTACAC	CAGGGCAGGT	CTAGCATTT	TTCATTTAGT	GTATGCTGC	CATTATCGCA	960
ACCACCTCG	GACTCTGGA	TTCCTCGCT	AGTTGAGGTC	CTGATGCTG	CTCCCTGGG	1020
GAGGTGAGGG	AGAGGCCCA	TGGTTCAATG	GGATCTGTGC	AGTTGTAACA	CATTAGGTGC	1080
TTAATAAACAA	GAAGCTGTGA	TGTTAAAAAA	AAAAAAAAAA			1119

(2) INFORMATION FOR SEQ ID NO:178:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 164 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Homo sapiens*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:178:

Met	Glu	Asn	Glu	Leu	Phe	Cys	Ser	Gly	Val	Leu	Val	His	Pro	Gln	Trp
1				5					10					15	
Val	Leu	Ser	Ala	Ala	His	Cys	Phe	Gln	Asn	Ser	Tyr	Thr	Ile	Gly	Leu
20					25				30						
Gly	Leu	His	Ser	Leu	Glu	Ala	Asp	Gln	Glu	Pro	Gly	Ser	Gln	Met	Val
35					40					45					
Glu	Ala	Ser	Leu	Ser	Val	Arg	His	Pro	Glu	Tyr	Asn	Arg	Pro	Leu	Leu
50					55					60					
Ala	Asn	Asp	Leu	Met	Leu	Ile	Lys	Leu	Asp	Glu	Ser	Val	Ser	Gly	80
65					70					75					
Asp	Thr	Ile	Arg	Ser	Ile	Ser	Ile	Ala	Ser	Gln	Cys	Pro	Thx	Ala	Gly
85										90					95
Asn	Ser	Cys	Leu	Val	Ser	Gly	Trp	Gly	Leu	Leu	Ala	Asn	Asp	Ala	Val
100									105					110	
Ile	Ala	Ile	Gln	Ser	Xaa	Thr	Val	Gly	Gly	Trp	Glu	Cys	Glu	Lys	Leu
115									120					125	
Ser	Gln	Pro	Trp	Gln	Gly	Cys	Thr	Ile	Ser	Ala	Thr	Ser	Ser	Ala	Arg
130									135					140	
Thr	Ser	Cys	Cys	Ile	Leu	Thr	Gly	Cys	Ser	Leu	Leu	Leu	Thr	Ala	Ser

145 150 155 160

- Pro Gly Thr Leu

(2) INFORMATION FOR SEQ ID NO:179:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 250 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:179:

CTGGAGTGC	TTGGTGTTC	AAGCCCTG	AGGAAGCAGA	ATGCACCTTC	TGAGGCACCT	60
CCAGCTGCC	CCGGCGGGG	GATGGAGGG	TCGGAGCAC	CTTGCCCCG	TGTGATTGCT	120
GCCAGGCACT	GTTCATCTCA	GCTTTCTGT	CCCTTGTCTC	CCGGCAAGCG	CTTCTGCTGA	180
AAGTTCATAT	CTGGAGCCTG	ATGCTTAAC	GAATAAAGGT	CCCATGCTCC	ACCCGAAAAAA	240
AAAAAAAAAA						250

(2) INFORMATION FOR SEQ ID NO:180:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 202 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:180:

ACTAGTCCAG	TGTGGTGAA	TTCATGTG	TGGGCCAA	CACATGGCT	ACCTTAAACA	60
TCACCCAGAC	CCCGCCCTG	CCCGTCGCC	ACGCTGCTG	TAACGACAGT	ATGATGCTTA	120
CCTCTGCTACT	CGAAAACAT	TTTATGAA	TAAATGATG	CTTCTTGTG	TATAAATGCC	180
TGATTTAAA	AAAAAAA	AA				202

(2) INFORMATION FOR SEQ ID NO:181:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 558 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:181:

TCCYTTGKT	NAGGTTKKG	AGACAMCK	AGACCTWAAN	CTGTGTACA	GACTTCYNG	60
ATGTTTAGG	CAGTGTAGT	AAATTCTYCG	TAATGATTCT	GTTATTACTT	TCCTNATTCT	120
TTATCTCTCT	TTCTCTGAA	GATTAATGAA	GTTGAAATT	GAGGTGGATA	AAATACAAAAAA	180
GGTAGTGTGA	TAGTAAAGT	ATCTAAGTGC	AGATGAAAGT	GTGTTATATA	TATCCATTCA	240
AAATTATGCA	AGTTAGTAAAT	TACTCAGGGT	TAACCTAAATT	ACTTTAATAT	GCTGTGAC	300
CTACTCTGTT	CCTTGCTAG	AAAAAATTAT	AAACAGGACT	TTGTTAGTT	GGGAAGCCAA	360
ATTGATAATA	TTCTATGTC.	AAAAAGTTG	GCTATACATA	AAATTATTAAG	AAATATGGAW	420

TTTATTCGG AGGAATATGG KGTCATTT ATGAATATTA CSCRGGATAG AWGTWTGAGT
 AAAAYCAGT TTGGTWAATA YGTWAATATG TCMTAAATAA ACAAKGCTTT GACTTATTTC
 CAAAAAAA AAAAAAAA 480
 540
 558

(2) INFORMATION FOR SEQ ID NO:182: (xi) SEQUENCE DESCRIPTION:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 479 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:182: (xi) SEQUENCE DESCRIPTION:

ACAGGGWITK GRGGATGCTA AGSCCCRGAG RWTYGTTGAG TCCAACCCIG GCTTWTITTC
 AGAGGGAAA ATGGGCCCTA AGAAGTACAG MSCATYTAGY TGTTGCGMTG GCACCCCTCG
 CSTCACACAG ASTCCCGAGT AGCTGGACT ACAGGCCAC AGTCACTGAA GCAGGGCCCTG
 TTWGCAATTC ACGTTGCAC CTCCAACTTA AACATTCTTC ATATGTGATG TCCCTTAGTCA
 CTAAGGTAA ACTTTCCAC CGAGAAAAGG CAACTTGTAGAT AAAATCTTAG AGTACTTCA
 TACTMTTCTA AGTCTCTTC CAGGCTCACT KKGAGTCCTM CYTGGGGTT GATAAGGANT
 NTCTCTGGC TTCTCAATA AARTCTCTAT YCATCTCAAG TTAAITTGG TACGCTARAA
 AWTGSTGARA AAATTTAAAT GTTCTGGTT MACTTTAAA AAAAAAAA AAAAAAAA 60
 120
 180
 240
 300
 360
 420
 479

(2) INFORMATION FOR SEQ ID NO:183:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 384 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:183:

AGGCAGGGAGC AGAACGTAAGA GCACAAAGCCC AAGAACAGATG GCAGTGCCAG CACTGGTCCC
 AGTACCCAGG CCAATAAACAG TGCCAGTGGC AGTGCAGAGCA CCAGTGGTGG CTTCAGTGGT
 GGTGCCAGCC TGACCCGACCT TCTCACATTGGGCTCTCG CTGGCCCTGG TGGAGCTGGT
 GGCAGCACCA GTGCGACTC TGTTGCGCTT GGTTCCTCTC ACAATGAGA TTTTAGATAT
 TGTTAACCTCT GCCAGCTTT CTCTCAAGC CAGGGTGCAT CCTCAGAAAC CTACTCAACA
 CAGCACTCTA GCCAGGCACT ATCAATCAAT TGAAGTTGAC ACTCTGCATT ARATCTATT
 GCCATTCAA AAAAAAAA AAAAA 60
 120
 180
 240
 300
 360
 384

(2) INFORMATION FOR SEQ ID NO:184:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 496 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:184:

ACCGAATTGG GACCCTGGC TTATAAGCGA TCATGTYNT CCRGTATKAC CTCACAGAGC 60

AGGGAGATCG AGTCTATACG CTGAAGAAAAT TTGACCCGAT GGGACAAACAG ACCTGCTCAG	120
CCCATCTGC TCGTTCTCC CCAGATGACA AATACTCTSG ACACCGAATC ACCATCAAAGA	180
AACGCCCTCAA GTGTGCTCATC ACCCAGCAAC CGGGCCCTGT CCTCTGAGGG TCCCTTAAC	240
TGATGCTTT TCTGCCACCT GTTACCCCTC GGAGACTCCG TAACCAAACCT CTTGGACTG	300
TGAGCCCTGA TGCCCTTTTG CCAGCCATAC TCTTTGGCAT CCAGTCTCTC GTGGCAGATG	360
ATTATGCTG TGTTGAGGCCAA TCATGGTGGC ATCACCCATA AAGGGAACAC ATTGACTG	420
TTTTCTCAT ATTTAAAT ACTACMAGAW TATTWMAGAW WAAATGAWTT GAAAAAACTST	480
AAAAAAAAA AAAAAA	496

(2) INFORMATION FOR SEQ ID NO:185:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 384 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:185:

GCTGGTAGCC TATGGGKGKG CCCACGGAGG GGCTCTGAG GCCACGGGRAC AGTGA	60
CAAGTATCYT GCGCSGCGTC TTCTACCGTC CCTACCTGCA GATCTTCGGG CAGATTCCCC	120
AGGAGGACAT GGACGTGGCC CTCATGGAGC ACAGAACTG YTCTGCGAG CCCGGCTCT	180
GGGCACACCC TTCTGGGGCC CAGGGGGCA CCTGGCTCTC CCAGATGAGC AACTGGCTGG	240
TGGTGTGCT CTCGTCATC TTCCCTGCTCG TGCCCAACAT CTCCTGGTC AACTTGCTCA	300
TTGCCATGTT CAGTTACACA TTGGCAAAAG TACAGGGCAA CAGCGATCTC TACTGGGAAG	360
GCGCAGCGTT ACCGCTCAT CGCG	384

(2) INFORMATION FOR SEQ ID NO:186:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 577 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:186:

GAGTTAGCTC CTCCACAAAC TTGTAGGAGT CGTCTGAGT GGCTCTCGC TTCAACCGC	60
TNCCATCTC ATACTGTAGG TTGCCACCA CYTCTGCGA TCTTGGGGCG GCNTAAATT	120
CCAGGAAACT CTCACCAAG TCACCGTGA TGAAAGCTGT GGGCTGGTTC TGTCTTCGGC	180
TCGGTGTGAA AGGATCTCCC AGAAGGAGTG CTGCATCTT CCCACACTTT TGATGACTTT	240
ATTGAGTGA TTCTGATGT CCAGCAGGAG GTTGTACCAAG CTCTCTGACA GTGAGGTAC	300
CAGCCCTATC ATGCCGTTGA MCGBTGCGGA GARCACCGAG CCTTGTGTGG GGGKKGAA	360
CTCACCCAGA TTCTGATTA CCAGAGAGCC GTGGCAAAAG ACATTGACAA ACTGCCAG	420
GTGGAAAAG AMCAMCTCT GGARGTGTCTN GCGCTCTCTC GTCMGTGTTGGT GGCACGGCTW	480
TCCTTTGAC ACACAAACAA GTTAAAGGCA TTTTCAGGCC CCAGAAANTT GTCATCATCC	540
AAGATNTCGC ACAGCACTNA TCCAGTTGGG ATTAAT	577

(2) INFORMATION FOR SEQ ID NO:187:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 534 base pairs
- (B) TYPE: nucleic acid

(C) STRANDEDNESS: sin

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 182; 100

AACATCTTCC	TGTATAATGC	TGTGTAATAT	CGATCCGATN	TITGCTGSGTG	AGAATYCATW	60
ACTKGAAAAA	GMAACATTAA	AGCCTGGACA	CTGGTATTAA	AATTCCACAT	ATGCAACACT	120
TTAACAGT	TGTCATCTG	CTCCCTYYNAC	TTTGTCTCATCA	CCAGCTCTGGG	AKAAAGGGTA	180
TCGCCCTATTG	ACACCTGTTA	AAAAGGGCGCT	AAGCATTTTT	GATTCAACAT	CTTTTTTTTT	240
GACACAAGTC	CGAAAAAAAGC	AAAAGTAAAC	AGTATTAYAT	TITGGTAGCCA	ATTCACATTTC	300
TTCATGGGAC	AGAGCCATTY	GATTAAAAAA	GCCTTATGCA	TAATATTGAG	CTTYGGAGC	360
TGATATTGAA	CGGGAAGAGT	AGCCCTTCTA	CTTCACAGCA	CACAATCCTC	TTTCATATTTG	420
GGATGTTNAC	NAAAGTWATC	TCTCTWACAG	ATGGATGCT	TITGTGGCA	TTCTGTTCTG	480
AGGATCTCCC	AGTTTATTCA	CCACTTGCAC	AGAAAGGCGT	TITCTTCCTC	AGGC	534

(2) INFORMATION FOR SEQ ID NO:186:

(i) SEQUENCE CHARACTERISTICS.

(A) LENGTH: 361 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

AGAACACCGT	ATCTCTAAA	ACAACCTCTC	ATACACTTG	GACCTAATT	TGTGTCG	60
TGTGTCG	CGCATATTAT	ATAGACAGGC	ACATCTTT	TACTTTG	AAAGCTTATG	120
CCCTTCTT	ATCTATATCT	GTGAAAGTT	TAATGATC	CCATAATGTC	TGGGGACCT	180
TGTCTTCTG	TGTAATGGT	ACTAGAGAAA	ACACCTATNT	TAGTGAATCA	TCTAGTTNGT	240
TTTATTCGAC	ATGAAGGAA	TTTCCAGATN	ACAAACACTNA	CAAACCTCC	CTKGACKARG	300
GGGGGAAAG	AAAAGAAAAA	CTGAMCATAA	RAAACATAW	CTCTGGAGA	ARTTGCATAA	360
ACAGAAATWR	GGTAGTATAT	TGAARNACAG	CATCTTAA	RMGTWTTKTT	WTTCCTCCCC	420
GCAAAACAA	TGTGACNGCT	TCCCCTTGG	TAATGCCAAG	TGTTTTTT	TATNATAAAA	480
CTGCCCCTC	ATTACATGTT	TNAAGTGGT	GTGGTGGGCC	AAAATATG	ATATGTTGAA	540
CTGACTGATA	AAGCTGTACA	ATAAACGCT	GTGCTTCAAA	AGCACACAG	TAATGTTGAC	600
ATGCTTAAAT	CACAAATGCT	AAATTCTTCA	TAATAATGTTG	CTAAAATACA	CTTGTGAACTA	660
TTTTCTGTN	TTTCCCGAACG	TGAGATNTTA	GATTTTATG	AGTATNAAGT	GGAAAANTAC	720
GAAAATAATA	ACATGGAAGA	AAAANAAA	AAAANAAA	AAA		780

(2) INFORMATION FOR SEC ID NO. 180

(i) SEQUENCE CHARACTERISTICS

(A) LENGTH OF 483 BASES

(A) LENGTH: 482 base pairs
(B) TYPE: nucleic acid

(B) TYPE: nucleic acid

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 100

```

TTTTTTTTT TTTGCGATN CTTACTATTTC ATTGCAGGGAN GTGGGGGTGT ATGACCGCAGA 60
CCCCGGGCT ATNAGAAAGCA AGAAAGGAAGG AAGGGGGCGCA CAGCCCGCTTG CTGAGCAACA 120
AAGCGGCTC TTGCTCTCTC TTGTCTGCTC TTGTGTCAGG CATCATGGGA TCTGGCTTCGGC 180

```

AAGGCAGGGG	CCACCACTCC	AGGGGTGGGA	ATACAGGGGG	TGGGAGNTGT	GCATAAGAAG	240
TGATAGGCAC	AGGCCACCCG	GTACAGACCC	CTCGGCTCCT	GACAGGTNGA	TTTCGACCAG	300
GTCATTGTC	CCTGCCAGG	CACAGCGTAN	ATCTGGAAA	GACAGAAATGC	TTTCCTTITC	360
AAATTGGCT	NGTCATNGAA	NGGGCANTT	TCCAANTING	GCTNGGTCTT	GGTACNCTTG	420
GTTCGGCCCA	GCTCCNCCTC	CAAAAANTAT	TCACCCNNCT	CCNAATTGCT	TGCGNGNNCC	480
CC						482

(2) INFORMATION FOR SEQ ID NO:190:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 471 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:190:

TTTTTTTTTT	TTTAAACAA	GTTTTCACA	ACAAAATTAA	TTAGAAGAAT	AGTGGTTTGT	60
AAAACCTCTG	CATCCAGTGA	GAACATACAT	ACACCACTATT	ACAGCTNGGA	ATGTNCTCCA	120
AATGTCCTGG	CAAATGATAC	AATGAAACCA	TTCACTCTTA	CACATGCGG	AAAAGAACAG	180
CGCTTTGAC	ATACATGCA	AAAAAAA	AGGGGGGGG	GACCATGTTG	ATTTAAATTT	240
TAAGTACTCA	TCACATACAT	TAAGCACACG	TCTCTACTCCA	GTCTAAATC	AGAACTGCNT	300
TGAAAAATT	CATGTATGCA	ATCCAAACCA	AAAGCTTNT	TGGTGTATCA	GANTNCTCTA	360
CTACATCNAC	CTTGATCATT	GGCAGGAACN	AAAAGTNTAA	ANACACNCGT	ACAAAAANAA	420
TCCTGTAATT	ANTTCAACCT	CCGTACNGAA	AAATNTNNNT	TATACACTCC	C	471

(2) INFORMATION FOR SEQ ID NO:191:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 402 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:191:

GAGGGATGAA	AGGTCTGTC	TASTGTCGGM	CTGTTGCGC	ACCAACTCTA	ACAAGTGTCT	60
GTCTTCACT	CACTGTCGT	AAGCTTTITA	ACCCAGACWG	TATCTTCATA	ATAAGAACAA	120
ATTCTTCAACC	AGTCACATCT	TCTAGGACT	TTTTGGATTG	AGTTAGTATA	AGCTCTTCCA	180
CTTCCTTGT	TAAGACTCA	TCTGGTAAAG	TCTTAAGTT	TGTAGAAAGG	AATTYATTCG	240
CTCGTTCTCT	AACAAATGTC	TCTCCTTGAA	GTATTTGGCT	GAACAACCCA	CCTAAAGTCC	300
CTTTGTGCA	CCATTAA	TATACCTTA	AGGGCATGK	TNCACTAGGT	TAATTTCTGC	360
AAGAGTCATC	TGTCTGCAA	AGTTGCGTTA	GTATATCTGC	CA		402

(2) INFORMATION FOR SEQ ID NO:192:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 601 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:192:

GAGCTCGGAT	CCAATAATCT	.TGTCTGAGG	GCACGCCACA	TATNCAGTGC	CATGGNAACT	60
GGCTCACCCC	ACATGGAGG	AGCATGGCGT	AGNTATATAA	GGTCATTCCC	TGAGTCAGAC	120
ATCTTCTTTT	GAATACCGTG	TGCCAAGTGC	TGGTGATTCT	YAACACACYT	CCATCCCGYT	180
CTTTTGTA	AAAATCTGGCA	CTTKTCTGGA	ACTAGCARGA	CATCACTTAC	AAATTCAACC	240
ACGAGACACT	TGAAGGTGT	AAACAAAGGA	YTCTTGCATT	GCTTTTGTG	CTCCGGGCAC	300
CAGTTGTCAT	TACTAACCCG	CTGGTTTGC	TCCATCACAT	TTGTGATCTG	AGCTCTGGA	360
TACATCTCT	GACAGTCTG	AAGAATCTCT	TCTTTTGTTT	CAAAGGCRC	TCTTGGTGCC	420
TGTTGGATCA	GGTTCCCAT	TCCCCAGTCY	AAATGTCACA	TGGCATATT	WACTTCCAC	480
AAAACATCTG	GATTTGAGGC	TCAGCAACAG	CAAATCCTGT	TCCGGCAT	GCTGCAAGAG	540
CCTCGATGTA	GCCGGCCAGC	GCCAAGGCAG	GCGCCGTGAG	CCCCACCAAGC	AGCGAAGACCA	600
G						601

(2) INFORMATION FOR SEQ ID NO:193:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 608 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:193:

ATACAGCCCCA	NATCCCCACA	CGAAGATGCG	CTTGTGACT	GAGAACCTGA	TCCGGTCACT	60
GGTCCCGCTG	TAGCCCCAGC	GACTCTCAC	CTGCTGAGG	CGTTGATGC	TGCACTCYTT	120
CCCAACGAG	GCAGMAGCG	GSCCCCGTC	TGAACTCCY	TGTCGCTTG	GGGTKGACGG	180
TKAAGTGCAG	GAAGAGGTG	ACCACCTCG	GGTCCACCA	GATGCCCGAC	TGTGCGGAC	240
CTGCAGCGAA	ACTCTCGAT	GGTCATGAGC	GGGAAGCGAA	TGAGGCCAG	GGCCCTTGGCC	300
AGAACCTTC	GCCTGTTTC	TGGCCTCAC	TGCACTGTG	GGCGCTGACA	CTCGGCCCTCG	360
GACCAAGCGGA	CAAACGGCT	TGAACAGCGG	CACCTCACGG	ATGCCAGTG	TGTCGGCTCG	420
CAGGAMMOSC	ACCACGCTGT	CCAGGTCAAT	TGCGGTGAAG	CCCTCCGGCG	GTRATGGCGT	480
CTGAGTGT	TTTGTGATG	TTCTCCAGGC	ACAGGCTGCG	CAGCTGCGGT	TCATCGAGA	540
GTCGCCCTG	C GTGAGCAGC	ATGAAGGCGT	TGTCGGCTCG	CAAGTCTTCT	TCAGGAACATC	600
CACGCAAT						608

(2) INFORMATION FOR SEQ ID NO:194:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 392 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:194:

GAACGGCTGG	ACCTTGCTC	GCATTGCTG	TGCTGGCAGG	GAATACCTTG	GCAAGCAGYT	60
CCAGTCCGAG	CAGCCCCAGA	CCGCTGCCG	CCGAGCTAA	GCCTGCCCT	GGCCTTCCCC	120
TCCGCCCTAA	TGCAAGACCA	GTAGTGGAG	CACTGTGTTT	AGAGTTAAGA	GTGAAACACTG	180
TTTGATTCTA	CTTGGAAATT	TCTCTCTGTTA	TATAGCTTT	CCCAATGCTA	ATTTCCAAC	240
AAACAACACA	AAATAACATG	TTTGCCTGTT	AACTGTATA	AAAGTAGGTG	ATTCTGTTAT	300
AAAGAAAAAT	ATTACTGTAA	CATATACTGC	TTGCAATTTC	TGTATTATT	GKTNCTSTGG	360
AAATAAAAT	AGTTTATTAA	GGTTGTCANT	CC			392

(2) INFORMATION FOR SEQ ID NO:195:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 502 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:195:

CCSTTKGAGG	GGTKAGGYKC	CAGTTYCCGA	GTGGAAGAAA	CAGGCCAGGA	GAAGTCGCGTG	60
CCGAGCTGAG	GCAGATGTTTC	CCACAGTGAC	CCCCAGAGCC	STGGGSTATA	GTYTCTGACC	120
CCTCNCAGG	AAAGACCACS	TTCTGGGAC	ATGGGCTGGA	GGGAGGACCC	TAGAGGCACCC	180
AAGGGAAGGC	CCCATTCTCCG	GGGSTTCTCC	CGAGGAGAA	GGGAAGGGG	TCTGCTGCCC	240
CCCCASAGG	AAGAGGCCCT	GAGTCTCTGG	ATCAGACAC	CCTTCACCTG	TATCCCCACA	300
CAAATGCAAG	CTCACCAAGG	TCCCCCTCTCA	GTCCCCCTTC	STACACCCCTG	AMCGGCCACT	360
GSCSCACACC	CCACCGAGAC	ACGCCAACCG	CCATGGGAR	TGTGCTCAAG	GARTCGCNGG	420
GCARCGTGG	CATCTNGTCC	CAGAAGGGGG	CAGAACCTCC	ATAGANGAAA	CTGARCMSTT	480
GCTNANAAAAA	AAAAAANAAA	AA				502

(2) INFORMATION FOR SEQ ID NO:196:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 665 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:196:

GTTACTTGG	TTTCATTTGC	ACCACTTAGT	GGATGTCACT	TAGAACCAATT	TTGTCTGCTC	60
CCTCTGGAAAG	CCTTGGCCAG	ACGGGACTTT	GTATTTGTTG	GAGAATAACT	GCTGAATT	120
WAGCTGTTTK	GAGTTGATTS	GCACCACTGC	ACCCCAACT	TCATATGAA	AACYANTTGA	180
ACTWATTATAT	TATCTTGAA	AAAGTATAAC	AATGAAAATT	TTGTTCATAC	TGTATTAKTC	240
AAAGTATGAG	AAAGCAAWA	GATATATATT	CTTTTATTAT	GTAAATTAT	GATTGCCATT	300
ATTAATCCGC	AAAATGGGA	GTGTTAGTTC	TTTTCACAGT	AATATATGCC	TTTTGTA	360
TCACTTGGTT	ATTTTATGTT	AAATGARITA	CAAATTCTT	AATTTAAGAR	AAATGGTATGT	420
WATATTATTTC	TCATTAAATT	CTTTCCTKGT	TTACGTWAT	TTTGAAGAGA	WTGCATGATT	480
TCTTGACAGA	AATCGATCTT	GATGCTGTGG	AACTAGTTTG	ACCCACATCC	CTATGACTTT	540
TCTCTTGAAT	GTATAAAAGGT	TGTAGCCCAT	CNAACTCTCAA	AGAAAAAAAT	GACCACATAC	600
TTTGCATCTC	GGCTGAATGT	TGGCATCTTA	TTCTAACTCC	AACTTTATAA	ACTAGCAAAN	660
AAAGTG						665

(2) INFORMATION FOR SEQ ID NO:197:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 492 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:197:

TTTTNTTTT	TTTTTTTTGC	AGGAAGGATT	CCATTATGG	TGGATGCATT	TTCACAAAT	60
ATGTTTATTG	GAGCGATCCA	TTATCAGTGA	AAAGTATCAA	GTGTTTATAA	NATTTTAGG	120
AAGGCAGATT	CACAGAACAT	GCTNGTCNGC	TTGCAGTTT	ACCTCGTANA	GATNACAGAG	180
AATTATAGTC	NAACCAACTA	ACNAGGAATT	TACTTTCAA	AAAGATTAAT	CCAAACTGAA	240
CAAATTCCTA	CCCTGAAACT	TACTCCATCC	AAATATTGGA	ATAANAGTCA	GCAGTGATAC	300
ATTCTCTCT	GAACTTTGA	TTTCTAGAA	AAATATGTA	TAGTGATCATG	GAAGAGCTCT	360
TGTTCAAAAG	TACACNAAG	CAATGTC	TTACCCATAGG	CCTTAATTCA	AACTTTGATC	420
CATTCTAC	CCATCACCGG	AGTCAATGCT	ACCTGGACA	CTTGTATT	GTTCATNCG	480
ANCNTGGCTT	AA					492

(2) INFORMATION FOR SEQ ID NO:198:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 478 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:198:

TTTNTTTTGN	ATTCANTCT	GTANNAANT	TTTCAATT	GTTTTATTANA	AAAATATNAA	60
TGNTNTCCACN	ACAAATCATN	TTACNTNAGT	AAAGGGCCAN	CTACATGTA	CAACATACAC	120
TGAGTATATT	TTGAAAAGGA	CAAGTTAAA	GTANACNCTA	ATTGCCGANC	ATANACACATT	180
TATACATGGC	TTGATGATA	TTTAGCACAG	CANAAAATGTA	GTGAGTTACC	AGAAANAAAT	240
NATATATGTC	AATCNGATTT	AAAGTACAAA	ACAGATCTCA	TGGTACATAN	CATCNCTGAG	300
GAGTTGTGTC	TTTATGTTTA	CTGAAAGTCA	ATGCATTC	TGTACAAAGA	GATGCCGCTA	360
AGCATTCTAG	TACCTCTACT	CCATGTTAA	GAATCCTACA	CTTATGTTA	CATATGTCNA	420
GGGTAAGAAT	TGTGTTAAGT	NAANTATGG	AGAGGTCCAN	GAGAAAATT	TGATNCAA	478

(2) INFORMATION FOR SEQ ID NO:199:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 482 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:199:

AGTGACTTGT	CCTCCAACAA	AACCCCTTGA	TCAAGTTGT	GGCACTGACA	ATCAGACCTA	60
TGCTAGTTCC	TGTCATCTAT	TCGCTACTAA	ATGCAGACTG	GAGGGGACCA	AAAAGGGCCA	120
TCAACTCCAG	CTGGATTATT	TTGGAGCCGTG	CAAATCTATT	CCTACTTGTAA	CGGACTTTGA	180
AGTGATTCTAG	TTTCTCTAC	GGATGAGAGA	CTGGCTCAAG	AAATATCCTCA	TGCACTT	240
TGAAGCCNAC	TCTGAACACG	CTGTTTACT	NAGATGAGAA	NCAGAGAAAT	AAAGTCNAGA	300
AAATTTACCT	GGGAGAAAAG	AGGCTTINTG	CTGGGGGACCA	TCCCTATGGA	CCTTCTCTTA	360
ANGGACTTTA	AGAANAAACT	ACCACATGTA	TGTGTTATCC	TGGTGCNNNG	CGGTTTANTG	420
AACNTNGACN	NCACCCCTNT	GGAATANANT	CTTGACNGCN	TCTGAACTT	GCTCCTCTGC	480
GA						482

(2) INFORMATION FOR SEQ ID NO:200:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 270 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:200:

CCGGCGCAAG	TGCAACTCCA	GCTGGGGCCG	TGCGGACGAA	GATTCTGCCA	GCAGTTGGTC	60
CGACTGGCAC	GACGGCGGG	GCGACAGTCG	CAGGTGCGAC	GCGGGCCCT	GGGGTCTTGC	120
AAGGCTGAGC	TGACGCCCA	GAGGTCCTGT	CACGCTCCAC	GACCTTGACG	CCGTGGGGGA	180
CAGGGGAAAC	AGAGCGGGGT	GAANGGGGA	GGCCTCGGGG	AGCCCCTCGG	GAAGGGCGGC	240
CCGAGAGATA	CGCAGGTGCA	GGTGGCCCO				270

(2) INFORMATION FOR SEQ ID NO:201:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 419 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:201:

TTTTTTTTT	TTTTGGAAATC	TACTGGGAGC	ACAGCAGGTC	AGCAACAAGT	T ^T ATTTTGC	60
GCTTACCAAGG	TAACAGGTTA	GGGCATGGTT	ACATGTTAG	GTCAACTTCC	TTTGTGTTG	120
TTGATTTGGT	TGTCTTTATG	GGGGCGGGGT	GGGGTAGGGG	AAANCAGAAC	ANAANTAAACA	180
TGGAGTGGGT	GCACCCCTCC	TGTAGAACCT	GGTTACNAAA	GCTTGGGGCA	GTTCACCTGG	240
TCTGTGACCC	TCATTTCTCT	GACATCATG	TTATTAGAAAG	TCAGGATATC	TTTTAGAGAG	300
TCCACTGTNT	CTGGAGGGAG	ATTAGGGTTT	CITGCCAANA	TCCAANAAA	ATCCACNTGA	360
AAAAGTTGGA	TGATNCANGT	ACNGAATACC	GANGGCATAN	TTCTCATANT	CGGTGGCCA	419

(2) INFORMATION FOR SEQ ID NO:202:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 509 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:202:

TTTNTTTTTT	TTTTTTTTT	TTTTTTTTT	TTTTTTTTT	TTTTTTTTT	TTTTTTTTT	60
TGGCACTTAA	TCCATTTTTA	TTTCAAARTG	TCTACAAANT	TTNAATNCNC	CATTATAACNG	120
GTNATTTTNC	AAAATCTAA	NNTTTATTCAA	ATTNNTAGCCA	AANTCCTTAC	NCAAAATNNAA	180
TACNCNCAAA	AATCAAAAT	ATACNTCT	TTTCAGCAAC	TTNGTTACAT	AAATTTAAAAA	240
AATATATACG	GCTGTTGTTT	TCAAAGTAC	ATTATCTTAC	CACTGCAAC	ATNTTTNNAA	300
GGAACTAAAA	TAACAAAAAA	CACTNCGCCA	AAGGTTAAAG	GGAAACACAA	ATTCTNTTTA	360
CAACANCNC	NATTATTTAA	ATCATATCTC	AAATCTTAGG	GGAAATATATA	CTTCACACNG	420
GGATCTTAAAC	TTTTACTNTCA	CTTTGTTTAT	TTTTTANAAA	CCATTGTTNT	GGGCCAACAA	480
CAATGGNAAT	NCNCNCNC	TGGACTAGT				509

(2) INFORMATION FOR SEQ ID NO:203:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 583 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:203:

TTTTTTTTT	T	TTTTTTTGTG	CCCCCTCTT	ATAAAAAAAC	AGTTACCA	TTATTTTACT		60
TACACATATT	T	ATTTTATAA	TTGGTATTAG	ATATTCAAA	GCGAGCTTT	AAATCAAAAC		120
TAAATGAA	C	CTGCCTT	TAGA	TACATAATTC	TTAGGAATT	GCTTAAAATC	TGCC	180
GAAATCTTC	T	TCTAGCTCTT	TTGAGTAA	ATTTTGACT	CTTGAA	AAAC	ATCC	240
ATTTCTCTG	T	TCTTTAAAT	TATCTTA	TCT	TTCATT	TTT	TCCCTAT	600
GCTCTCTAG	C	CCTCAT	TCC	TAGCTCTT	CTACTAT	TAAGTGG	CTT	300
AGGGAA	A	GAAGAGAGA	ATGGCACA	AAACAAACAT	TTTATATTC	TATTTCTACC		360
TACGTTAATA	A	AAATAGCAT	TTG	GAAGCC	AGCTCAA	AG	GGCTT	420
TCCATTITAG	T	TCAC	AAAC	ATATCNAA	TGCCAGA	ATG	CAAAGGTT	480
ATTCAAAAGC	A	TAATATAA	GA	TTACAT	TTG	GTGAC	ATT	540
								583

(2) INFORMATION FOR SEQ ID NO:204:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 589 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:204:

TTTTTTTTNT	T	TTTTTNC	TCT	TTTTT	TTGANA	ATGA	GGATCGAG	TT	60
TTTCACTCTC	T	AGATAGGGC	ATGAAGAAA	CTCAT	CTTC	CAGCTT	AA	ATACATCA	120
AATCTCTAT	A	GCTATCAT	ATTTTA	AGTT	AAACTA	ATGA	GTC	ACTG	180
TGAAGGAA	C	CTGTCATC	TCT	CTCAT	TAGTT	TATA	TCAG	TACTA	240
TGAGAGGTT	T	TTCTTCTCTA	TTTACAC	ATA	TATT	CCAT	TGA	ATTG	300
ATTTTCATG	A	AAACTAGAAA	ATATG	TNT	TTT	TCAT	AG	AGAGAAGAGA	360
CATTACAAA	C	CTGCTCA	TGTT	GTAA	GNTT	TATC	T	ACATATINAG	420
CTAATACAAA	T	TCACATTAC	NGACNAGCAA	TTAATA	AAAC	GAAGTAC	CCAG	TAAATATCC	480
AAAATAATAA	A	AGGAACATT	TTT	AGCCTG	GTATA	ATTAG	CTAAT	CACT	540
TTATTNAGAA	G	TGAATT	CACA	TATT	CCNTAG	CCC	ACACA	ATGG	589

(2) INFORMATION FOR SEQ ID NO:205:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 545 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:205:

TTTTTNNTTT TTTTTTCAGT AATAATCAGA ACAATATTAA TTTTTATATT TAAAATTCA	60
AGAAAAGTGC CTTACATTTA ATAAAAGTTT GTTTCTCAA GTGATCAGAG GAATTAGATA	120
TNGCTTGAA CACCAATATT AATTGAGGA AAATACCCA AAATACATTA AGTAAATTAT	180
TTAACATCAT AGAGCTTGTAA AGTGAAAAGA TAAAATTGAA CCTCAGAAC TCTGAGCATT	240
AAAAATCCAC TATTAGCAAA TAAATTTACTA TGGAACITCTT GCTTTAAATT TGTTGATGAAT	300
ATGGGGTGC ACTGGTAAC CAACACATTC TGAAGGATAC ATTACTTAGT GATAGATTTCT	360
TATGACTTT GCTANATNAC GTGGATATGA GTTGACAACT TTCTCTTCT TCAATCTTTT	420
AAGGGCNGA NGAAATGAGG AAGAAAGAA AAGGATTAGC CATACTGTTT TTTCTATNGG	480
AAGGATTAGA TATGTTCTT TTGCAAATAT TAAAAAATA ATAATGTTA CTACTAGTGA	540
ACCC	545

(2) INFORMATION FOR SEQ ID NO:206:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 487 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:206:

TTTTTTAGTC AAGTTCTNA TTTTTATATT AATTAAGTC TTGGTCATT	60
CATTATTAG CTCTGCACT TACATATTAA TAAATTAAGAA ACGTINNTAG ACAACTGNTNA	120
CAATTATAAA ATGTAAGGTG CCATTATTGA GTANATATAT TCCTCCAAGA GTGGATGTGT	180
CCCTCTCCC ACCAATTAAT GAANCAGCAA CATTAGTTA ATTITTTAG TAGATNATAC	240
ACTGCTGCAA ACGCTTAATC TCTCTCCCAT CCCCATGNG ATATGTTGTA TATGTTGAG	300
TTGGTNAGAA TGCATCANCA ATCTNACAAAT CAACACGAA ATGAAAGCTAG CGNTGGCCTT	360
TGGTGAAGAA TAGACTGTG CTGTCGAAT CAAATGATCT GACCTATCCT CGGTGGCAAG	420
AACTCTCGA ACCGCTTCTT CAAAGCNC TGCCACATT GTGGCCTCTN TTGCACTTGT	480
TTCAAAA	487

(2) INFORMATION FOR SEQ ID NO:207:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 332 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:207:

TGAATTGGCT AAAAGACTGC ATTTTANAA CTGAACTC TTATTCTTT CCTTTAAAAA	60
TACATAGCAT TAAATCCAA ATCCTATTAA AAGACCTGAC AGCTTGAGAA GGTCACTACT	120
GCATTATAG GACCTTCTGG TGTTCTGCT GTTACANTTTG AANTCTGACA ATCCCTGANA	180
ATCTTGTCA GCAGAGGAGG TAAAAGGTG TGATTTCAGA CAGAGGAANA ACACAGGCCA	240
GAATAGAGG GGCAGAGCTT ACTGAGCTTG TCCACTGGAG GGCTCATGGG TGGGACATGG	300
AAAAGAAGGC AGCCTAGGCC CTGGGAGCC CA	332

(2) INFORMATION FOR SEQ ID NO:208:

(i) SEQUENCE CHARACTERISTICS:

129

- (A) LENGTH: 524 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:208:

AGGGCGTGGT	GGGGAGGGGG	TTACTGTGTT	GTCTCAGTAA	CAATAAAATAC	AAAAAGACTG	60
GTGTGTTCCC	GGCCCCATCC	AACCAAGAAG	TTGATTTCCTC	TTGTGTGCAG	AGTGACTGTGAT	120
TTAAAGGAC	ATGGAGCTTG	TTCACATGTC	ACAATGTCAC	AGTGTAAGG	GCACACTCAC	180
TCCCGCGTGA	TTCACATTTC	GCAACCAACA	ATAGCTCATG	AGTCATACT	TGTAATAACT	240
TTTGCAGAA	TACTTNTTGA	AACTTGCAGA	TGATAACTAA	GATCAGAT	ATTTCACAAA	300
GTAAATAGAA	GTGGGTCTATA	ATATAATTA	CCTGTTACCA	TCAGCTTCCA	TTTACAAGTC	360
ATGAGCCCCAG	ACACTGACAT	CAAACAAAGC	CCACTTAGAC	TCCTCACCAC	CAGTCTGTCC	420
TGTCATCAGA	CAGGGGGCTG	TCACCTTGAC	CAAATTCTCA	CCAGTCACAT	ATCTATCCAA	480
AAACCATTAC	CTGATCCACT	TCCCGTAAATG	CACCACTTGTG			524

(2) INFORMATION FOR SEQ ID NO:209:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 159 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:209:

GGGTGAGGAA	ATCCAGAGTT	GCCATGGAGA	AAATTCCAGT	GTCAGCATTTC	TTGCTCTTGT	60
TGGCCCTCTC	CTACACTCTG	GCCAGAGATA	CCACAGCTAA	ACCTGGGCC	AAAAGGACA	120
CAAAGGACTC	TCGACCCAAA	CTGCCCCAGA	CCCTCTCCA			159

(2) INFORMATION FOR SEQ ID NO:210:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 256 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:210:

ACTCCCTGGC	AGACAAAGGC	AGAGGAGAGA	GCTCTGTGTTAG	TTCTGTGTTG	TTGAATGCCC	60
ACTGAATTTC	TTTCCACTTG	GACTATTACA	TGCCANTTGA	GGGACTTAATG	AAAAAACGTTA	120
TGGGGAGATT	TTANANCAATT	TANGTNTGTA	AAATGGGAGA	CTGGGGCAGG	CGGGAGAGAT	180
TTGCAGGGTG	NAATGGGAN	GGCTGGTTG	TTANATGAAC	AGGGACATAG	GAGGTAGGCA	240
CCAGGATGCT	AAATCA					256

(2) INFORMATION FOR SEQ ID NO:211:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 264 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:211:

ACATTGTTTT	TGGAGATAA	AGCATTGAGA	GAGCTCTCCT	TAACGTGACA	CAATGGAAGG	60
ACTGGAAAC	ATACCCACAT	CTTTGTCTG	GGGATAATT	TTCTGATAAA	GTCTTGCTGT	120
ATATTCAAGC	ACATATGTTA	TATATTATTC	AGTTCCATAG	TTATAGCTTA	GTAAAGGAGA	180
GGGGAGATAC	ATTCTNGAACG	AGGACTGAAA	GAATACTCA	AGTNNGAAAA	CAGAAAAAGA	240
AAAAAAGGAG	CAAATGAGAA	GCCT				264

(2) INFORMATION FOR SEQ ID NO:212:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 328 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:212:

ACCCAAAAAT	CCAATGCTGA	ATATTTGGCT	TCATTATTC	CANATTCTTT	GATTGTCAAA	60
GGATTAAATG	TTGTCCTCAG	TTGGGCAACTT	CAGITTAGGAC	CTAAGGATGC	CAGCCGGCAG	120
GTATTATATAT	GCAGCAACAA	TATTCAAGGG	CGACACACGG	TTATTGAACT	TGCCCGCCAG	180
TINAATTCTCA	TTCCCATGTA	CTGGGATCC	TTATCATCG	CCAGAGAGAT	TGAAAATTAA	240
CCCCTACNAC	TCTTACTCTT	CTGGANAGG	CCAGTGGTGG	TAGCTATAAG	CTTGCCACACA	300
TTTTTTTTTC	CTTATTCTCT	TTGTCAGA				328

(2) INFORMATION FOR SEQ ID NO:213:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 250 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:213:

ACTTATGAGC	AGAGCGGACAT	ATCCNAGTGT	AGACTGAATA	AAACTGAATT	CTCTCCAGTT	60
TAAAGCATTG	CTCACTGAGG	GGATAGAAGT	GACTGCCAGG	AGGGAAAGTA	AGCCAAGGCT	120
CATTATGCCA	AGGANATAT	ACATTCAAT	TCTCCAACT	TCTCTCTCAT	TCCAAGAGTT	180
TTCAATAATT	GCATGAAACCT	GCTGATAANC	CATGTTAANA	AACAAATATC	TCTCTNACCT	240
TCTCATCGGT						250

(2) INFORMATION FOR SEQ ID NO:214:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 444 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:214:

```

ACCCAGAACAT CAATGCTGAA TATTGGCTT CATTATTCCC AGATTCITGT ATTGTCAAAG    60
GATTAAATGT TGTCTCAGCT TGGGCACCTTC AGTTGACCC TAAGGATGCC AGCGCCGAGG   120
TTTATATATG CAGCAACAT ATTCAAGGG CACACACGGT TATTGAACTT GCCCCGAGT    180
TGAATTCATC TCCCATGAC TTGGGATCTT TATCATCAGC CANAGAGATT GAAAATTTAC  240
CCCTACGACT CTITACTCTC TGGAAGGGC CAGTGGTGT AGCTATAAGC TTGGCCACAT  300
TTTTTTCC TTTATTCCTT TGTCAGAGAT CGCATTCATC CATATGCTAN AAACCAACAG  360
AGTGAATTTT ACAAAATCC TATAGANATT GTGAATAAAA CCTTACCTAT AGTTGGCATT  420
ACTTTGCTC CCCTAATATA CCTC

```

444

(2) INFORMATION FOR SEQ ID NO:215:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 366 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:215:

```

ACTATGAGC AGAGGAGCAT ATCCAAGTGT ANACTGAATA AACTGAATT CTCTCCAGTT 60
TAAGGCATTG CTCACTGAGG GGATAGAGT GACTGCGAGG AGGGAAGTA AGCCAAGGCT 120
CATTATGCC AAGGANATAT ACATTCATC TCTTCAACT TCTTCCATT TCCAAGAGTT 180
TTCAATATTG CGATCAACT GCTGATAAGC CATGTGGAGA ACAAAATATC TCTCTGACCT 240
TCTCATCGGT AAGCAGAGGC TGAGGCAAC ATGGACCATA GCGAANAAAA AACITAGTAA 300
TCCAAGCTGT TTTCTACACT GTAACCAGGT TTCCAACCAA GGTGGAATC TCCTATACCT 360
GOTGCC

```

366

(2) INFORMATION FOR SEQ ID NO:216:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 260 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:216:

```

CTGTATAAAC AGAACTCCAC TGCGANGAGGG AGGGCGGGC CAGGAGAATC TCCGCTTGTG 60
CAAGCAGGG GCCTAAGGG GGTCTCCACA CTGCTNNTAA GGGCTNTNC ATTTTTTTAT 120
TAATAAAAAG TNNAAAAGGC CTCTTCTCAA CTTTTTTCCC TTNGGCTGGA AAATTTAAAA 180
ATCAAAATTT TCCTNAAGTT NTCAAGCTAT CATATATACT NTATCCGTAA AAACCAACAT 240

```

AATTCTTCCT TCCCTGCC

260

(2) INFORMATION FOR SEQ ID NO:217:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 262 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:217:

ACCTACGGG GTAAGTTTAAATGTATA ATTTCGAAA NAGGAACCCA TATAATTGTA	60
TCTTGCTTAT AATTTCTAT TTAAATAAGG AAATAGCAAA TTGGGGTGGG GGGAAATGTAG	120
GGCATCTTAC AGTTTGAGCA AAATGCATT AAATGTGGAA GGACAGCACT GAAAAATTAA	180
ATGAATAATC TGTATGATTA TATGTCTCTA GAGTAGATT ATAATTAGCC ACTTACCCCA	240
ATATCCCTCA TGCTGTGAA GT	262

(2) INFORMATION FOR SEQ ID NO:218:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 205 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:218:

ACCAAGGTGG TGCAATTACCG GAANTGGATC AANGACACCA TCGTGGCCAA CCCCTGAGCA	60
CCCCATCAA CTCCCTTTG TAGTAAACTT GGAAACCTTGG AAATGACCAAG GCACAGACTC	120
AGGCTCCCC AGTTCTACT ACCTTTGTCC TTANGINTNA NGTCCAGGGT TGCTAGGAAA	180
ANAAATCAGC AGACACAGGT GTAAA	205

(2) INFORMATION FOR SEQ ID NO:219:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 114 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:219:

TACTGTTTG TCTCAGTAAC AATAAATACA AAAAGACTGG TTGTGTTCCG GCCCCATCCA	60
ACCAAGAAGT TGATTCTCT TGTGTGCAGA GTGACTGATT TTAAAGGACA TGGA	114

(2) INFORMATION FOR SEQ ID NO:220:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 93 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:220:

```
ACTAGCCAGC ACAAAAGGCA GGGTAGGCTG AATTGCTTTC TGCTCTTTAC ATTTCTTTTA
AAATAAGCAT TTAGTGCTCA GTCCCTACTG AGT
```

60
93

(2) INFORMATION FOR SEQ ID NO:221:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 167 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:221:

```
ACTANTGCA GGTGCGCACA AATATTGTC GATATTCCCT TCATCTTGGG TTCCATGAGG
TCTTTGCCC AGCCTGTGGC TCTACTGTAG TAAGTTCTG CTGATGAGGA GCCAGNATGC
CCCCCACTAC CTTCCCTGAC GCTCCCCANA AATCACCCAA CCTCTGT
```

60
120
167

(2) INFORMATION FOR SEQ ID NO:222:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 351 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:222:

```
AGGGCAGTGTG GCGGAGGGCG GTACTGACCT CATTAGTAGG AGGATGCAATTCTGGCACCC
GTTCTTCACC TCCCTCCCAA TCCCTAAAGG GCCATACCTC ATAAGCTCAA CAACAGCTAA
ATGTTCTGCTG AATTAAGGGA TGGATGAAAA AAATTAATAAA TGAATTTTG CATAATCCAA
TTTTCTCTTT TATATTCTA GAAGAAGTTT CTTTGAGGCT ATTAGATCCC GGGAAATCTTT
TAGGTGAGCA TGATTAGAGA GCTTGTAGGT TGCTTTACA TATATCTGGC ATATTGAGT
CTCGTATCAA AACAAATAGAT TGGTAAAGGT GGTATTATTG TATTGATAAG T
```

60
120
180
240
300
351

(2) INFORMATION FOR SEQ ID NO:223

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 383 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:223:

AAAACAAACA AACAAAAAAA ACAATTCTTC ATTCAAGAAAA ATTATCTTAG GGACTGATA	60
TGGTAATTAT GGTCAATTTC ATWRTRTTK TGGGCATTTC CTTACATTGT CTTGACAAAGA	120
TTAAATATGTC TGTGCCAAA TTTTGATTTT TATTTGGAGA CTTCCTTATCA AAAGTAATGC	180
TGCCRAAGGA AGCTAAAGGA ATTAGTAGTG TTCCCMTCAC TTGTTGGAG TGTCCTATTG	240
TAAGAGATT TGTAGTCCTG GAATGACAAT TATATTTAA CTTTGGTGGG GGAAANAGTT	300
ATAGGACAC AGTCTTCACT TCTGATACCT GTAAATTAAAT CTTTTATTCG ACTTGTITTG	360
ACCATTAAGC TATATGTTA AAA	383

(2) INFORMATION FOR SEQ ID NO:224:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 320 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:224:

CCCCCTGAAGG CTTCTTGTAA GAAATAGTA CAGTTAACAC CAATAGGAAAC AACAAAAAGA	60
AAAAGTTTGT GACATTGTAG TAGGGAGTGT GTACCCCTTA CTCCCCATCA AAAAAAAAT	120
GGATACATGG TTAAAGGATA RAAGGGCAAT ATTTTATCAT ATGTTCTAAA AGAGAAGGAA	180
GAGAAATAC TACTTTCTCR AAATGGAAAC CCTTAAAGGT GCTTTGATAC TGAAAGGACAC	240
AAATGTGCCG GTCCCATCTTC CTTTARAGTT GCATGACTTG GACACGGTAA CTGTTGCAGT	300
TTTARACTCM GCATTGTGAC	320

CLAIMS

1. A method for detecting prostate cancer in a patient, comprising:

- (a) contacting a biological sample obtained from the patient with a binding agent which is capable of binding to a polypeptide, the polypeptide comprising an immunogenic portion of a prostate protein or a variant thereof, wherein said protein comprises an amino acid sequence encoded by a DNA molecule having a sequence selected from the group consisting of nucleotide sequences recited in SEQ ID Nos: 2-3, 5-107, 109-111, 115-171, 173-175, 177 and 179-224, the complements of said nucleotide sequences and variants of said nucleotide sequences; and

(b) detecting in the sample a protein or polypeptide that binds to the binding agent, thereby detecting prostate cancer in the patient.

2. The method of claim 1 wherein the binding agent is a monoclonal antibody.

3. The method of claim 2 wherein the binding agent is a polyclonal antibody.

4. A method for monitoring the progression of prostate cancer in a patient, comprising:

- (a) contacting a biological sample obtained from the patient with a binding agent that is capable of binding to a polypeptide, said polypeptide comprising an immunogenic portion of a prostate protein or a variant thereof, wherein said protein comprises an amino acid sequence encoded by a DNA molecule having a sequence selected from the group consisting of nucleotide sequences recited in SEQ ID Nos: 2-3, 5-107, 109-111, 115-171, 173-175, 177 and 179-224, the complements of said nucleotide sequences and variants of said nucleotide sequences;

(b) determining in the sample an amount of a protein or polypeptide that binds to the binding agent;

(c) repeating steps (a) and (b); and

(d) comparing the amount of polypeptide detected in steps (b) and (c) to monitor the progression of prostate cancer in the patient.

5. A monoclonal antibody that binds to a polypeptide comprising an immunogenic portion of a prostate protein or a variant thereof, wherein said protein comprises an amino acid sequence encoded by a DNA molecule having a sequence selected from the group consisting of nucleotide sequences recited in SEQ ID Nos: 2-3, 8-29, 41-45, 47-52, 54-65, 70, 73, 74, 79, 81, 87, 90, 92, 93, 97, 103, 104, 107, 109-111, 115-160, 171, 173-175, 177, 181, 188, 191, 193, 194, 198, 203, 204, 207, 209-211, 220, 222-224, the complements of said nucleotide sequences variants of said nucleotide sequences.

6. A method for inhibiting the development of prostate cancer in a patient, comprising administering to the patient a therapeutically effective amount of a monoclonal antibody according to claim 5.

7. The method of claim 6 wherein the monoclonal antibody is conjugated to a therapeutic agent.

8. A method for detecting prostate cancer in a patient comprising:

(a) obtaining a biological sample from the patient;

(b) contacting the sample with at least two oligonucleotide primers in a polymerase chain reaction, wherein at least one of the oligonucleotides is specific for a DNA molecule encoding a polypeptide comprising an immunogenic portion of a prostate protein or of a variant thereof, said protein comprising an amino acid sequence encoded by a DNA molecule having a sequence selected from the group consisting of nucleotide sequences recited in SEQ ID Nos: 2-3, 5-107, 109-111, 115-171, 173-175, 177 and 179-224, the complements of said nucleotide sequences variants of said nucleotide sequences; and

(c) detecting in the sample a DNA sequence that amplifies in the presence of the oligonucleotide primers, thereby detecting prostate cancer.

9. The method of claim 8, wherein at least one of the oligonucleotide primers comprises at least about 10 contiguous nucleotides of a DNA molecule having a sequence selected from SEQ ID Nos: 2-3, 5-107, 109-111, 115-171, 173-175, 177 and 179-224.

10. A diagnostic kit comprising:

- (a) one or more monoclonal antibodies of claim 5; and
- (b) a detection reagent.

11. A diagnostic kit comprising:

- (a) one or more monoclonal antibodies that bind to a polypeptide encoded by a DNA molecule having a nucleotide sequence selected from the group consisting of SEQ ID Nos: 5-7, 30-40, 46, 53, 66-69, 71, 72, 75-78, 80, 82-86, 88, 89, 91, 94-96, 98-102, 105, 106, 161-170, 179, 180, 182-187, 189, 190, 192, 195-197, 199-202, 205, 206, 208, 212-219, 221, the complements of said sequences and variants of said nucleotide sequences; and
- (b) a detection reagent.

12. The kit of claims 10 or 11 wherein the monoclonal antibodies are immobilized on a solid support.

13. The kit of claim 12 wherein the solid support comprises nitrocellulose, latex or a plastic material.

14. The kit of claims 10 or 11 wherein the detection reagent comprises a reporter group conjugated to a binding agent.

15. The kit of claim 14 wherein the binding agent is selected from the group consisting of anti-immunoglobulins, Protein G, Protein A and lectins.

16. The kit of claim 14 wherein the reporter group is selected from the group consisting of radioisotopes, fluorescent groups, luminescent groups, enzymes, biotin and dye particles.

17. A diagnostic kit comprising at least two oligonucleotide primers, at least one of the oligonucleotide primers being specific for a DNA molecule encoding a polypeptide comprising an immunogenic portion of a prostate protein or a variant thereof, said protein comprising an amino acid sequence encoded by a DNA molecule having a sequence selected from the group consisting of nucleotide sequences recited in SEQ ID Nos: 2-3, 5-107, 109-111, 115-171, 173-175, 177 and 179-224, the complements of said nucleotide sequences and variants of said nucleotide sequences.

18. A diagnostic kit of claim 17 wherein at least one of the oligonucleotide primers comprises at least about 10 contiguous nucleotides of a DNA molecule having a sequence selected from SEQ ID Nos: 2-3, 5-107, 109-111, 115-171, 173-175, 177 and 179-224.

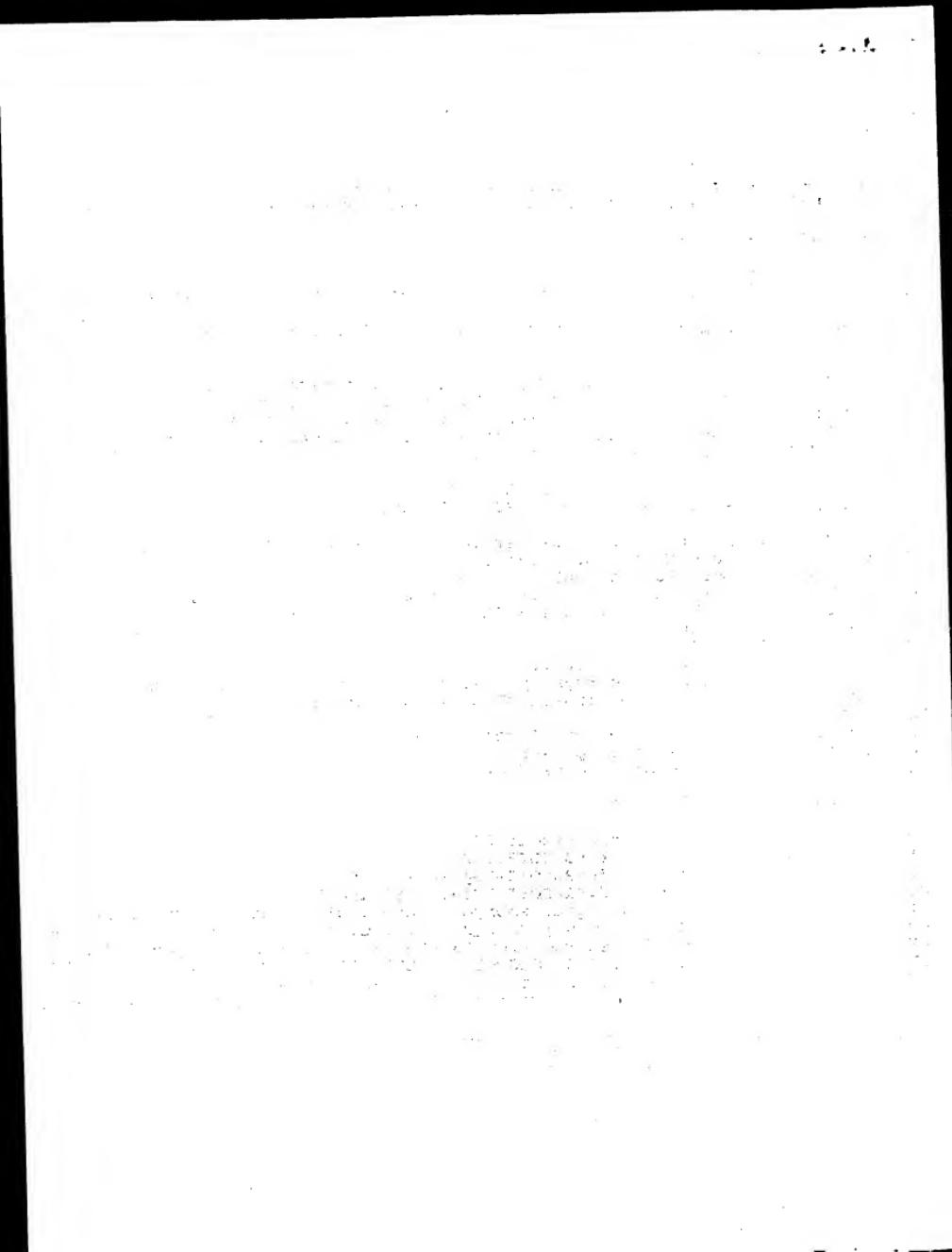
19. A method for detecting prostate cancer in a patient, comprising:
(a) obtaining a biological sample from the patient;
(b) contacting the biological sample with an oligonucleotide probe specific for a DNA molecule encoding a polypeptide comprising an immunogenic portion of a prostate protein or a variant thereof, said protein comprising an amino acid sequence encoded by a DNA molecule having a sequence selected from the group consisting of nucleotide sequences recited in SEQ ID Nos: 2-3, 5-107, 109-111, 115-171, 173-175, 177 and 179-224, the complements of said nucleotide sequences and variants of said nucleotide sequences; and
(c) detecting in the sample a DNA sequence that hybridizes to the oligonucleotide probe, thereby detecting prostate cancer in the patient.

20. The method of claim 19 wherein the oligonucleotide probe comprises at least about 15 contiguous nucleotides of a DNA molecule having a sequence selected from the group consisting of SEQ ID Nos: 2-3, 5-107, 109-111, 115-171, 173-175, 177 and 179-224.

21. A diagnostic kit comprising an oligonucleotide probe specific for a DNA molecule encoding a polypeptide comprising an immunogenic portion of a prostate

protein or a variant thereof, said protein comprising an amino acid sequence encoded by a DNA molecule having a sequence selected from the group consisting of nucleotide sequences recited in SEQ ID Nos: 2-3, 5-107, 109-111, 115-171, 173-175, 177 and 179-224, the complements of said nucleotide sequences variants of said nucleotide sequences.

22. The diagnostic kit of claim 21, wherein the oligonucleotide probe comprises at least about 15 contiguous nucleotides of a DNA molecule having a sequence selected from the group consisting of SEQ ID Nos: 2-3, 5-107, 109-111, 115-171, 173-175, 177 and 179-224.



a301248_0001.Dna /rev
nest_Rod12:Mmaa36804

D MMAA36804 standard; RNA; EST; 627 BP.
C AA536804;
V AA536804.1
T 31-JUL-1997 (Rel. 52, Created)
T 03-MAR-2000 (Rel. 62, Last updated, Version 2)
E vj88f09.rl Knowles Solter mouse 2 cell *Mus musculus* cDNA clone IMAGE:9442c
E 3', mRNA sequence.
W EST.
S *Mus musculus* (house mouse)
C Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia
C Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
N [1]
P 1-627
A Marra M., Hillier L., Allen M., Bowles M., Dietrich N., Dubuque T.,
A Geisel S., Kucaba T., Lacy M., Le M., Martin J., Morris M.,
A Schellenberg K., Steptoe M., Tan F., Underwood K., Moore B., Theising B.,
A Wylie T., Lennon G., Soares B., Wilson R., Waterston R.;
RT "The WashU-HHMI Mouse EST Project";
U Unpublished.
R RZPD; IMAGp998C182349; IMAGp998C182349.
R RZPD; IMAGp998C182349Q0; IMAGp998C182349Q0.

C On Sep 12, 1996 this sequence version replaced gi:1292316.
C Contact: Marra M/Mouse EST Project
C WashU-HHMI Mouse EST Project
C Washington University School of MedicineP
C 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
C Tel: 314 286 1800
C Fax: 314 286 1810
C Email: mouseest@watson.wustl.edu
C This clone is available royalty-free through LLNL ; contact the
C IMAGE Consortium (info@image.llnl.gov) for further information.
C MGI:541057
C Possible reversed clone: polyT not found
C High quality sequence stop: 469.
FH Key Location/Qualifiers
FT source 1. .627
FT /db_xref="taxon:10090"
FT /db_xref="ESTLIB:862"
FT /db_xref="RZPD:IMAGp998C182349"
FT /db_xref="RZPD:IMAGp998C182349Q0"
FT /note="Organ: embryo; Vector: pBluescribe (modified);
FT Site_1: MluI; Site_2: SalI; Cloned unidirectionally from
FT mRNA prepared from 13,500 2-cell stage embryos. Primer:
FT SalI(dt): 5'-CGGTCGACCGTCGACCGTTTTTTTTTT-3'. cDNAs
FT were cloned into the MluI/SalI sites of a modified
FT pBluescribe vector using commercial linkers (NEB). Avera
FT insert size: 1.2 kb."
FT /organism="Mus musculus"
FT /strain="B6D2 F1/J" . . .

SCORES Init1: 581 InitN: 581 Opt: 661 z-score: 767.4 E(): 0
 70.9% identity in 278 bp overlap

	329	319	309	299	289	279
a301248_000	GGCCCTCTAGACTCGAGCGGCCGTCGNCCAGGAGATATTACCTCAGGAAATAGAT					
maa36804	GCTAAGGATGTATGTTACCAGTGCTATTCA	GAGGATCCTCACCCCTGGGAAACTGAT				
	150	160	170	180	190	200
	269	259	249	239	229	219
a301248_000	GCATCCAGCAACTATACTCCCCAAGATCCTGCAAGAAATGAAATCCACAGTGATAAGGA					
maa36804	ATGTTCACTAACATCAGACCACAGTCTTCTGC	AAATAATGAGATTAATGATGAAAGTGAA				
	210	220	230	240	250	260
a301248_000	209	199	189	179	169	159
maa36804	CCTGTCCTTACCTACATGACCAGCTGTCA	AGGAACTTCTAAAGAGTTCCATTGTCATT				
	270	280	290	300	310	320
a301248_000	149	139	129	119	109	99
maa36804	GAGGCTGTGAATACACGTGAAGGTTCTGTGGGCCAGCAAAC	TACATACCCAGACCTCAGAA				
	330	340	350	360	370	380
a301248_000	89	79	69	59	49	39
Mmaa36804	GATCAAACACTGCTGATAAAACCAAGTTCTGACTCCA	AAAGACCCAGCAGATCAAATACA				
	390	400	410	420	430	440
a301248_000	29	19	9			
Mmaa36804	ACAAATATTTCTTCATTTACTAGTGAGGTTG					
	450	460	470	480	490	500

a301248_0001.Dna
mhtg4:Ac016957

D AC016957 standard; DNA; HTG; 195002 BP.
C AC016957;
V AC016957.8
T 14-DEC-1999 (Rel. 62, Created)
T 02-JUN-2000 (Rel. 63, Last updated, Version 10)
E Homo sapiens clone RP11-50I19, WORKING DRAFT SEQUENCE, 47 unordered pieces
W HTG; HTGS_DRAFT; HTGS_PHASE1.
S Homo sapiens (human)
C Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia;
C Eutheria; Primates; Catarrhini; Hominidae; Homo;
N [1]
P 1-195002--
A Muzny D.M., Adams C., Bailey M., Barbaria J., Blankenburg K., Bodota B.,
A Bouck J., Bowie S., Brooks A., Buhay C., Buniac C., Burkett C., Burrows J.,
A Carter M., Chacko J., Chen Z., Cox C., David R., Delgado O., Deshazo D.,
A Ding Y., Domah-Rashid N., Dugan-Rocha S., Durbin K.J., Fernandez C.,
A Ferraguto D., Forcum-Tansey J., Frantz P., Ganesh R., Gorrell J.H.,
A Gorrell L.L., Guevara W., Harris K., Hernandez J., Hodgson A., Hogues M.,
A Holloway C., Hosak H., Jackson L.E., Jackson L., Jia Y., Jones M.,
A Kelly S., Kondejewski N., Kong Y., Kovar C., Leal B., Li Z., Lichatoge O.,
A Liu J., Liu W., Logan O., Lozado R.J., Lu J., Lucier R., Martin R.,
A Martinez C., McLeod M.P., Mei G., Morgan M., Morris S., Nash S., Nelson A,
A Nguyen R., Nguyen N., Nguyen S., Oswal G., Parish B., Paxton S., Payton B
A Perez L., Pu L.L., Quiles M., Reiter D., Rives M., Samuel S., Say J.,
A Scherer S., Shah E., Shen H., Simon M., Sparks A., Stamps A., Sucgang R.,
A Tabor P., Taylor T., Vasquez L., Vinson R., Vo Q., Wahbah M.,
A Watlington S., Weinstock G., Weinstock I.R., Williamson A., Worley K.,
A Wren J., Wrenford G., Yu W., Zhou X., Nelson D., Gibbs R.;
RT "Direct Submission";
RL Unpublished.
RN [2]
RP 1-195002
RA Worley K.C.;
RT ;
RL Submitted (09-DEC-1999) to the EMBL/GenBank/DDBJ databases.
RL Human Genome Sequencing Center, Department of Molecular and Human Genetics
RL Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
CC On May 30, 2000 this sequence version replaced gi:8025078.
CC -- Genome Center
CC Center: Baylor College of Medicine
CC Center code: BCM
CC Web site: <http://www.hgsc.bcm.tmc.edu/>
CC Contact: hgsc-help@bcm.tmc.edu
CC -- Project Information
CC Center project name: HMUV
CC Center clone name: RP11-50I19
CC -- Summary Statistics
CC Sequencing vector: M13; L08821
CC Chemistry: Dye-primer Bodipy: 9% of reads
CC Chemistry: Dye-terminator Big Dye: 91% of reads . . .

SCORES Init1: 1390 Initn: 1390 Opt: 1390 z-score: 1821.2 E(): 0
 100.0% identity in 278 bp overlap

a301248_000	CAACCTCACTAGTAAATGAAAAGAAATTGTAAATTGTATTGTATCTGCTGCTGGG	10	20	30	40	50	
c016957	GGAAATATTCCTTCATTTGCTGAGCTTAATATTGTAAATTGTATTGTATCTGCTGGG	27060	27070	27080	27090	27100	27110
a301248_000	TCTTGGAGTCAGAACACTGGTTTATCAGCAGTTGATCTCTGAGGTCTGATATGTAGTT	60	70	80	90	100	110
c016957	TCTTGGAGTCAGAACACTGGTTTATCAGCAGTTGATCTCTGAGGTCTGATATGTAGTT	27120	27130	27140	27150	27160	27170
a301248_000	TGCTGGCCCACAGAACCTTCACGTGTATTCAACGCCAATGCCATAAGGAAACTCTTT	120	130	140	150	160	170
c016957	TGCTGGCCCACAGAACCTTCACGTGTATTCAACGCCAATGCCATAAGGAAACTCTTT	27180	27190	27200	27210	27220	27230
a301248_000	AGAAGTTCTGACAGCTGGTCATGTAGGTATAAGACAGGTGCCTTATCACTGTGGATTCA	180	190	200	210	220	230
c016957	AGAAGTTCTGACAGCTGGTCATGTAGGTATAAGACAGGTGCCTTATCACTGTGGATTCA	27240	27250	27260	27270	27280	27290
a301248_000	TTTCTTGCGAGGATCTGGGGAGTATAGTTGCTGGATGCATCTATTCTGAGGGTAAATA	240	250	260	270	280	290
c016957	TTTCTTGCGAGGATCTGGGGAGTATAGTTGCTGGATGCATCTATTCTGAGGGTAAATA	27300	27310	27320	27330	27340	27350
a301248_000	TCCTCCTGGNCACGCGGCCGCTCGAGCTAGAGGGCCCTTAAACCCGCTGATCAGCC	300	310	320	330	340	350
c016957	TCCTCCTGAATAGCAGCTGACGAGCACGTATCGTTAGCTGTGCTTTTCAGTGGCATGC	27360	27370	27380	27390	27400	27410

a301248_0001.Dna
msyn:Af060226

D AF060226 standard; circular DNA; SYN; 5771 BP.
C AF060226;
V AF060226.1
T 06-MAY-1998 (Rel. 55, Created)
T 16-AUG-2000 (Rel. 64, Last updated, Version 2)
E Eukaryotic expression vector pCR3.1mBCL-XL, complete sequence.
W .
S Eukaryotic expression vector pCR3.1mBCL-XL
C artificial sequence; vectors.
N [1]
P 1-5771
A Pirtskhalashvili G., Shurin G.V., Gambotto A., Esche C., Wahl M.,
A Yurkovetsky Z.R., Robbins P.D., Shurin M.R.;
T "Transduction of dendritic cells with Bcl-xL increases their resistance to
T prostate";
J. Immunol. 165(4):1956-1964 (2000).
RN [2]
RP 1-5771
RA Gambotto A., Pagliano O., Shurin M., Robbins P.D.;
RT ;
RL Submitted (17-APR-1998) to the EMBL/GenBank/DDBJ databases.
RL Vector Core Facility, University of Pittsburgh, 300 Technology Drive,
RL Pittsburgh, PA 15219, USA
RH Key Location/Qualifiers
FH source 1. .5771
FT /db_xref="taxon:75965"
FT /organism="Eukaryotic expression vector pCR3.1mBCL-XL"
FT promoter 1. .596
FT /note="CMV"
FT promoter 638. .657
FT /note="T7; priming site also"
FT CDS 747. .1448
FT /codon_start=1
FT /note="BALB/c form"
FT /product="murine BCL-XL"
FT /protein_id="AAC15799.1"
FT /translation="MSQSNRELVVDFLSYKLSQKGYSWSQFSDVEENRTEAPEETEA
FT ETPSAINGNPSPWHLADSPAVNGATGHSSLDAREVIPMAAVKQALREAGDEFELRYR
FT FSDLTSQLHITPGTAYQSFEQVNVELFRDGVNWGRIVAFFSGGALCVESVDKEMQV
FT SRIASWMATYLNDHLEPWIQENGGWDTFVDLYGNNAAAESRKQERFNRWFLTGMTV
FT misc_feature VVLLGSLFSRK"
FT 1524. .1541
FT /note="pCR3.1 reverse priming site"
FT rep_origin 1827. .2500
FT CDS /note="ColE1"
FT complement(3082. .3870)
FT /codon_start=1
FT /product="neomycin/kanamycin resistance protein"
FT /protein_id="AAC15800.1"

CORES Init1: 427 Initn: 457 Opt: 427 z-score: 591.6 E(): 5.9e-25
96.6% identity in 89 bp overlap

a301248_000 280 290 300 310 320 330
TTCCTGAGGGTAAATATCCTCTGGNCACGCCGCGCTCGAGTCTAGAGGGCCCGTTTA

f060226 AGCCGAATTCTGCAGATATCCAGCACAGTGCGGCCGCTCGAGTCTAGAGGGCCCGTTTA

1450 1460 1470 1480 1490 1500
340 350 360 370 380 390

a301248_000 AACCCGCTGATCAGCCTCGACTGTGCCCTCTANTTGCCANCCATNTGTTGTTGCCCTC

f060226 AACCCGCTGATCAGCCTCGACTGTGCCCTCTAGTTGCCAGCCATCTGTTGTTGCCCTC

1510 1520 1530 1540 1550 1560
1570 1580 1590 1600 1610 1620

f060226 CCCCGTGCCTTCCTGACCCCTGGAGGTGCCACTCCACTGTCCCTTCTAATAAAATGA

i301248_0001.Dna
mpatent:Ax001326

) AX001326 standard; DNA; UNC; 7108 BP.
c AX001326;
v AX001326.1
r 10-MAR-2000 (Rel. 63, Created)
t 10-MAR-2000 (Rel. 63, Last updated, Version 1)
e Sequence 38 from Patent EP0892047.

w .
s unidentified
c unclassified.
n [1]

p 1-7108

a Fleckenstein B.P., Ensser A.D.;
"Human and murine semaphorin L";
l Patent number EP0892047-A/38, 20-JAN-1999.
l HOECHST MARION ROUSSEL DE GMBH (DE).
m Key Location/Qualifiers

ft source 1..7108
ft /db_xref="taxon:32644"
ft /organism="unidentified"

pt exon 1..7108
sq Sequence 7108 BP; 1617 A; 1970 C; 1875 G; 1646 T; 0 other;

SCORES Init1: 427 InitN: 457 Opt: 427 z-score: 590.7 E(): 5.4e-25
96.6% identity in 89 bp overlap

280 290 300 310 320 330

Sa301248_000 TTCCCTGAGGGTAAATATCCTCCTGGNCAGCGCGGCCGCTCGAGTCTAGAGGGCCGTTTA

Ax001326 TCATCATCATTGAGTTTATCCAGCACAGTGGCGGCCGCTCGAGTCTAGAGGGCCGTTTA
2620 2630 2640 2650 2660 2670

Sa301248_000 AACCCGCTGATCAGCCTCGACTGTGCCCTCTANITGCCANCCATNTGTGTGTTTGCCCCCT

Ax001326 AACCCGCTGATCAGCCTCGACTGTGCCCTCTAGTTGCCAGCCATCTGTGTGTTTGCCCCCTC
2680 2690 2700 2710 2720 2730

Ax001326 CCCCGTGCCTCCTTGACCCCTGGAAAGGTGCCACTCCCACGTGCTTCTAATAAAAATGA
2740 2750 2760 2770 2780 2790

D X02662 standard; DNA; 7108 BP.
 C X02662;
 T 07-MAY-1999 (first entry)
 E EP-892047 Seq ID 38.
 W Semaphorin L; human; immunosuppressant; anti-inflammatory; gene therapy;
 W organ transplantation; inflammation therapy; immunotherapy; agonist;
 W immunomodulatory; antagonist; ss.
 S Homo sapiens.
 N EP892047-A2.
 D 20-JAN-1999.
 F 06-JUL-1998; 98EP-0112470.
 R 11-FEB-1998; 98DE-1005371.
 R 09-JUL-1997; 97DE-1029211.

'A (HMRI) HOECHST MARION ROUSSEL DEUT GMBH.
 'I Ensser A, Fleckenstein B;
 'R WPI; 1999-083564/08.

'T New semaphorin L proteins - used as immunosuppressants and
 antiinflammatory agents in organ transplants, inflammation therapy,
 immunotherapy and gene therapy

'S Disclosure; Page 96-100; 135pp; German.

'C This invention describes a novel human semaphorin L protein. This protein
 or its encoding DNA are useful as immunosuppressants and/or
 anti-inflammatory agents in organ transplantation, inflammation therapy,
 immunotherapy and gene therapy. The DNA can be used to produce knock-out
 or knock-in animals for research purposes. The proteins or DNA can be

'C used to search for the corresponding receptors or to screen for
 immunomodulatory agonists or antagonists.

'Q Sequence 7108 BP; 1617 A; 1970 C; 1875 G; 1646 T; 0 other;

SCORES Init1: 427 Initn: 457 Opt: 427 z-score: 590.7 E(): 5.4e-25
 96.6% identity in 89 bp overlap

280 290 300 310 320 330
 Sa301248_000 TTCTGAGGGTAAATATCCCTCGGNCAGCGGGCGCTCGAGTCTAGAGGGCCCGTTA
 X02662 TCATCATCATGAGTTTATCCAGCACAGTGCGGCCGCTCAGTCTAGAGGGCCCGTTA
 2620 2630 2640 2650 2660 2670

340 350 360 370 380 390
 Sa301248_000 AACCCGCTGATCAGCTCGACTGTGCCCTCTANTTGCCANCCATNTGTTGTTGCCCCCT
 X02662 AACCCGCTGATCAGCTCGACTGTGCCCTCTAGTTGCCAGCCATCTGTTGTTGCCCCCTC
 2680 2690 2700 2710 2720 2730
 X02662 CCCCGTGCCTTCCTTGACCCCTGGAAAGGTGCACTCCCACGTGCTTTCTAATAAAATGA
 2740 2750 2760 2770 2780 2790

Same as AF 060226
 SA 181782

